

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

<130> P2830P1C62

<150> 09/946374
<151> 2001-09-04

<150> 60/098716
<151> 1998-09-01

<150> 60/098723
<151> 1998-09-01

<150> 60/098749
<151> 1998-09-01

<150> 60/098750
<151> 1998-09-01

<150> 60/098803
<151> 1998-09-02

<150> 60/098821
<151> 1998-09-02

<150> 60/098843
<151> 1998-09-02

<150> 60/099536
<151> 1998-09-09

<150> 60/099596
<151> 1998-09-09

<150> 60/099598
<151> 1998-09-09

<150> 60/099602
<151> 1998-09-09

<150> 60/099642
<151> 1998-09-09

<150> 60/099741
<151> 1998-09-10

<150> 60/099754
<151> 1998-09-10

<150> 60/099763
<151> 1998-09-10

<150> 60/099792
<151> 1998-09-10

<150> 60/099808
<151> 1998-09-10

<150> 60/099812
<151> 1998-09-10

<150> 60/099815
<151> 1998-09-10

<150> 60/099816
<151> 1998-09-10

<150> 60/100385
<151> 1998-09-15

<150> 60/100388
<151> 1998-09-15

<150> 60/100390
<151> 1998-09-15

<150> 60/100584
<151> 1998-09-16

<150> 60/100627
<151> 1998-09-16

<150> 60/100661
<151> 1998-09-16

<150> 60/100662
<151> 1998-09-16

<150> 60/100664
<151> 1998-09-16

<150> 60/100683

<151> 1998-09-17

<150> 60/100684
<151> 1998-09-17

<150> 60/100710
<151> 1998-09-17

<150> 60/100711
<151> 1998-09-17

<150> 60/100848
<151> 1998-09-18

<150> 60/100849
<151> 1998-09-18

<150> 60/100919
<151> 1998-09-17

<150> 60/100930
<151> 1998-09-17

<150> 60/101014
<151> 1998-09-18

<150> 60/101068
<151> 1998-09-18

<150> 60/101071
<151> 1998-09-18

<150> 60/101279
<151> 1998-09-22

<150> 60/101471
<151> 1998-09-23

<150> 60/101472
<151> 1998-09-23

<150> 60/101474
<151> 1998-09-23

<150> 60/101475
<151> 1998-09-23

<150> 60/101476
<151> 1998-09-23

<150> 60/101477
<151> 1998-09-23

<150> 60/101479
<151> 1998-09-23

<150> 60/101738
<151> 1998-09-24

<150> 60/101741
<151> 1998-09-24

<150> 60/101743
<151> 1998-09-24

<150> 60/101915
<151> 1998-09-24

<150> 60/101916
<151> 1998-09-24

<150> 60/102207
<151> 1998-09-29

<150> 60/102240
<151> 1998-09-29

<150> 60/102307
<151> 1998-09-29

<150> 60/102330
<151> 1998-09-29

<150> 60/102331
<151> 1998-09-29

<150> 60/102484
<151> 1998-09-30

<150> 60/102487
<151> 1998-09-30

<150> 60/102570
<151> 1998-09-30

<150> 60/102571
<151> 1998-09-30

<150> 60/102684
<151> 1998-10-01

<150> 60/102687
<151> 1998-10-01

<150> 60/102965
<151> 1998-10-02

<150> 60/103258
<151> 1998-10-06

<150> 60/103314
<151> 1998-10-07

<150> 60/103315
<151> 1998-10-07

<150> 60/103328

<151> 1998-10-07

<150> 60/103395
<151> 1998-10-07

<150> 60/103396
<151> 1998-10-07

<150> 60/103401
<151> 1998-10-07

<150> 60/103449
<151> 1998-10-06

<150> 60/103633
<151> 1998-10-08

<150> 60/103678
<151> 1998-10-08

<150> 60/103679
<151> 1998-10-08

<150> 60/103711
<151> 1998-10-08

<150> 60/104257
<151> 1998-10-14

<150> 60/104987
<151> 1998-10-20

<150> 60/105000
<151> 1998-10-20

<150> 60/105002
<151> 1998-10-20

<150> 60/105104
<151> 1998-10-21

<150> 60/105169
<151> 1998-10-22

<150> 60/105266
<151> 1998-10-22

<150> 60/105693
<151> 1998-10-26

<150> 60/105694
<151> 1998-10-26

<150> 60/105807
<151> 1998-10-27

<150> 60/105881
<151> 1998-10-27

<150> 60/105882
<151> 1998-10-27

<150> 60/106023
<151> 1998-10-28

<150> 60/106029
<151> 1998-10-28

<150> 60/106030
<151> 1998-10-28

<150> 60/106032
<151> 1998-10-28

<150> 60/106033
<151> 1998-10-28

<150> 60/106062
<151> 1998-10-27

<150> 60/106178
<151> 1998-10-28

<150> 60/106248
<151> 1998-10-29

<150> 60/106384
<151> 1998-10-29

<150> 60/108500
<151> 1998-10-29

<150> 60/106464
<151> 1998-10-30

<150> 60/106856
<151> 1998-11-03

<150> 60/106902
<151> 1998-11-03

<150> 60/106905
<151> 1998-11-03

<150> 60/106919
<151> 1998-11-03

<150> 60/106932
<151> 1998-11-03

<150> 60/106934
<151> 1998-11-03

<150> 60/107783
<151> 1998-11-10

<150> 60/108775

<151> 1998-11-17
<150> 60/108779
<151> 1998-11-17
<150> 60/108787
<151> 1998-11-17
<150> 60/108788
<151> 1998-11-17
<150> 60/108801
<151> 1998-11-17
<150> 60/108802
<151> 1998-11-17
<150> 60/108806
<151> 1998-11-17
<150> 60/108807
<151> 1998-11-17
NO<150> 60/108848
NO<151> 1998-11-18
NO<150> 60/108849
NO<151> 1998-11-18
NO<150> 60/108850
NO<151> 1998-11-18
NO<150> 60/108851
NO<151> 1998-11-18
NO<150> 60/108852
NO<151> 1998-11-18
NO<150> 60/108858
NO<151> 1998-11-18
<150> 60/108867
<151> 1998-11-17
<150> 60/108904
<151> 1998-11-18
<150> 60/108925
<151> 1998-11-17
<150> 60/113296
<151> 1998-12-22
<150> 60/114223
<151> 1998-12-30
<150> 60/129674
<151> 1999-04-16

<150> 60/141037
 <151> 1999-06-23

 <150> 60/144758
 <151> 1999-07-20

 <150> 60/145698
 <151> 1999-07-26

 <150> 60/162506
 <151> 1999-10-29

 <150> 09/218517
 <151> 1998-12-22

 <150> 09/284291
 <151> 1999-04-12

 <150> 09/403297
 <151> 1999-10-18

 <150> 09/872035
 <151> 2001-06-01

 <150> 09/882636
 <151> 2001-06-14

 <150> PCT/US99/00106
 <151> 1999-01-05

 <150> PCT/US99/20111
 <151> 1999-09-01

 <150> PCT/US99/21194
 <151> 1999-09-15

 <150> PCT/US99/28313
 <151> 1999-11-30

 <150> PCT/US99/28551
 <151> 1999-12-02

 <150> PCT/US99/30095
 <151> 1999-12-16

 <150> PCT/US00/00219
 <151> 2000-01-05

 <150> PCT/US00/00376
 <151> 2000-01-06

 <150> PCT/US00/03565
 <151> 2000-02-11

 <150> PCT/US00/04342
 <151> 2000-02-18

 <150> PCT/US00/05004

<151> 2000-02-24
<150> PCT/US00/05841
<151> 2000-03-02
<150> PCT/US00/06884
<151> 2000-03-15
<150> PCT/US00/13705
<151> 2000-05-17
<150> PCT/US00/14042
<151> 2000-05-22
<150> PCT/US00/14941
<151> 2000-05-30
<150> PCT/US00/15264
<151> 2000-06-02
<150> PCT/US00/23328
<151> 2000-08-24
<150> PCT/US00/23522
<151> 2000-08-23
<150> PCT/US00/30873
<151> 2000-11-10
<150> PCT/US00/30952
<151> 2000-11-08
<150> PCT/US00/32678
<151> 2000-12-01
<150> PCT/US01/06520
<151> 2001-02-28
<150> PCT/US01/06666
<151> 2001-03-01
<150> PCT/US01/17800
<151> 2001-06-01
<150> PCT/US01/19692
<151> 2001-06-20
<150> PCT/US01/21066
<151> 2001-06-29
<150> PCT/US01/21735
<151> 2001-07-09
<160> 477
<210> 1
<211> 43
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Sequence - Artificial

<400> 1

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 2

<211> 41

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-41

<223> Sequence - Artificial

<400> 2

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 3

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 3

ccaatcgccc ggtgcggtgg tgcagggctc cgggctagtc atggcgctccc 50

cgtctcggag actgcagact aaaccagtca ttacttggtt caagagcgtt 100

ctgctaactc acacttttat tttctggatc actggcggtta tccttcttgc 150

agttggcatt tggggcaagg tgagcctgga gaattacttt tctcttttaa 200

atgagaaggc caccaatgtc ccttcgtgc tcattgctac tggtagcgtc 250

tattattcttt tgggcacctt tgggtgtttt gctacctgcc gagcttctgc 300

atggatgcta aaactgtatg caatgtttct gactctcgtt tttttggtcg 350

aactggtcgc tgccatcgta ggatttggtt tcagacatga gattaagaac 400

agctttaaga ataattatga gaaggctttg aagcagtata actctacagg 450

agattataga agccatgcag tagacaagat ccaaaatacg ttgcattggt 500

gtggtgtcac cgattataga gattggacag atactaatta ttactcagaa 550

aaaggatttc ctaagagttg ctgtaaaactt gaagattgta ctccacagag 600

agatgcagac aaagtaaaca atgaagggtt ttttataaag gtgatgacca 650

ttatagagtc agaaatggga gtcgttgacg gaatttcctt tggagttgct 700

tgcttccaac tgattggaat ctttctogcc tactgccwct ctcggtccat 750

aacaaataac cagtatgaga tagtgtaacc caatgtatct gtgggcctat 800
tcctctctac ctttaaggac atttagggtc cccoctgtga attagaaagt 850
tgcttggtg gagaaactgac aacactactt actgatagac caaaaaacta 900
caccagtagg ttgattcaat caagatgtat gtagacctaa aactacacca 950
ataggtgat tcaatcaaga tccgtgctcg cagtgggctg attcaatcaa 1000
gatgtatgtt tgctatgttc taagtccacc ttctatccca ttcattgtag 1050
atcgttgaaa ccctgtatcc ctctgaaaca ctggaagagc tagtaaattg 1100
taaatagaagt 1110

<210> 4
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-42
<223> Signal Peptide

<220>
<221> TRANSMEM
<222> 19-42, 61-83, 92-114, 209-230
<223> Transmembrane Domains

<220>
<221> misc feature
<222> 69-80, 211-222
<223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>
<221> misc feature
<222> 75-81, 78-84, 210-216, 214-220, 226-232
<223> N-Myristoylation Site.

<220>
<221> misc feature
<222> 134-138
<223> N-Glycosylation Site.

<220>
<221> misc feature
<222> 160-168, 160-169
<223> Tyrosine Kinase Phosphorylation Site.

<220>
<221> unsure
<222> 233
<223> unknown amino acid

<400> 4
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250

1	5	10	15
Cys Phe Lys Ser Val	Leu Leu Ile Tyr Thr	Phe Ile Phe Trp Ile	
20	25	30	
Thr Gly Val Ile	Leu Leu Ala Val Gly	Ile Trp Gly Lys Val Ser	
35	40	45	
Leu Glu Asn Tyr	Phe Ser Leu Leu Asn	Glu Lys Ala Thr Asn Val	
50	55	60	
Pro Phe Val Leu	Ile Ala Thr Gly Thr	Val Ile Ile Leu Leu Gly	
65	70	75	
Thr Phe Gly Cys	Phe Ala Thr Cys Arg	Ala Ser Ala Trp Met Leu	
80	85	90	
Lys Leu Tyr Ala	Met Phe Leu Thr Leu	Val Phe Leu Val Glu Leu	
95	100	105	
Val Ala Ala Ile	Val Gly Phe Val Phe	Arg His Glu Ile Lys Asn	
110	115	120	
Ser Phe Lys Asn	Asn Tyr Glu Lys Ala	Leu Lys Gln Tyr Asn Ser	
125	130	135	
Thr Gly Asp Tyr	Arg Ser His Ala Val	Asp Lys Ile Gln Asn Thr	
140	145	150	
Leu His Cys Cys	Gly Val Thr Asp Tyr	Arg Asp Trp Thr Asp Thr	
155	160	165	
Asn Tyr Tyr Ser	Glu Lys Gly Phe Pro	Lys Ser Cys Cys Lys Leu	
170	175	180	
Glu Asp Cys Thr	Pro Gln Arg Asp Ala	Asp Lys Val Asn Asn Glu	
185	190	195	
Gly Cys Phe Ile	Lys Val Met Thr Ile	Ile Glu Ser Glu Met Gly	
200	205	210	
Val Val Ala Gly	Ile Ser Phe Gly Val	Ala Cys Phe Gln Leu Ile	
215	220	225	
Gly Ile Phe Leu	Ala Tyr Cys Xaa Ser	Arg Ala Ile Thr Asn Asn	
230	235	240	
Gln Tyr Glu Ile	Val		
245			

<210> 5
 <211> 1218
 <212> DNA
 <213> Homo sapiens

 <400> 5
 cccacgcgtc cggcgccgtg gcctcgcgtc catctttgcc gttctctcgg 50

<220>
 <221> misc_feature
 <222> 18-24, 32-38, 34-40, 35-41, 51-57
 <223> N-Myristoylation Site.

<220>
 <221> misc_feature
 <222> 22-26, 50-54, 113-117
 <223> Casein Kinase II Phosphorylation Site.

<400> 6
 Met Ile Val Phe Gly Trp Ala Val Phe Leu Ala Ser Arg Ser Leu
 1 5 10 15
 Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe
 20 25 30
 Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile
 35 40 45
 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
 50 55 60
 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
 65 70 75
 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
 80 85 90
 His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu
 95 100 105
 Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys
 110 115

<210> 7
 <211> 756
 <212> DNA
 <213> Homo sapiens

<400> 7
 ggacagagggc gctgtccacc cgggggcggtg ggagtgaggt accagattca 50
 gcccatattgg ccccgacgcc tctgttctcg gaatccgggt gctgcggatt 100
 gaggtcccggt ttcttaacgg actgcaagat ggaggaaggg gggaacctag 150
 gaggcctgat taagatggtc catctactgg tcttgtcagg tgcctggggc 200
 atgcaaattgt gggtgacctt cgtctcaggc ttctgtcttt tccgaagcct 250
 tccccgacat accttcggac tagtgacagag caaactcttc ccttctact 300
 tccacatctc catgggctgt gccttcatca acctctgcat ctgggcttca 350
 cagcatgctt gggctcagct cacattctgg gaggccagcc agctttacct 400
 gctgttctctg agccttacgc tggccactgt caacgcccgcg tggtgtggaac 450

cccgcaccac agctgccatg tgggccctgc aaaccgtgga gaaggagcga 500
 ggcctgggtg gggaggtacc aggcagccac caggggtcccg atccctaccg 550
 ccagctgcga gagaaggacc ccaagtacag tgctctccgc cagaatttct 600
 tccgctacca tgggctgtcc tctctttgca atctgggctg cgtcctgagc 650
 aatgggctct gtctogctgg ccttgccctg gaaataagga gcctctagca 700
 tgggccctgc atgctaataa atgcttcttc agaaatgaaa aaaaaaaaaa 750
 aaaaaa 756

<210> 8
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-24
 <223> Signal Peptide

<220>
 <221> misc_feature
 <222> 4-10, 5-11, 47-53, 170-176, 176-182
 <223> N-Myristoylation Site.

<220>
 <221> misc_feature
 <222> 44-85
 <223> G-protein Coupled Receptors Proteins.

<220>
 <221> misc_feature
 <222> 54-65
 <223> Prokaryotic Mmembrane Lipoprotein Lipid Attachment Site.

<220>
 <221> misc_feature
 <222> 82-86
 <223> Casein Kinase II Phosphorylation Site.

<220>
 <221> TRANSMEM
 <222> 86-103, 60-75
 <223> Transmembrane Domain

<220>
 <221> misc_feature
 <222> 144-151
 <223> Tyrosine Kinase Phosphorylation Site.

<400> 8
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His
 1 5 10 15

Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr
 20 25 30
 Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr
 35 40 45
 Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile
 50 55 60
 Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln
 65 70 75
 His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr
 80 85 90
 Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp
 95 100 105
 Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val
 110 115 120
 Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln
 125 130 135
 Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr
 140 145 150
 Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser
 155 160 165
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
 170 175 180
 Gly Leu Ala Leu Glu Ile Arg Ser Leu
 185

<210> 9

<211> 1508

<212> DNA

<213> Homo sapiens

<400> 9

aattcagatt ttaagcccat tctgcagtgga aatttcacga actagcaaga 50
 ggacaccatc ttcttggtatt atacaagaaa ggagtgtacc tatcacacac 100
 agggggaaaa atgctctttt ggggtgctagg cctcctaata ctctgtggtt 150
 ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200
 tacattttta tcaactggatg tgactcgggc ttggaaact tggcagccag 250
 aacttttgat aaaaagggat ttcatgtaat cgctgcctgt ctgactgaat 300
 caggatcaac agctttaag gcagaaacct cagagagact togtactgtg 350
 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400

<222> 36-47, 108-113, 166-171,198-203, 207-212

<223> N-myristoylation Sites.

<220>

<221> misc_feature

<222> 39-42

<223> Glycosaminoglycan Attachment Site.

<220>

<221> TRANSMEM

<222> 136-152

<223> Transmembrane Domain

<220>

<221> misc_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
125 130 135

Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
140 145 150

Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
170 175 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315
Pro Lys Ala Val														

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
 gcgggctggt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50
 gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggcggg 100
 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct totacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcatc agctggaggg 650

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
agtgcacatg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
gtgtccaggc ccttcagtga gtggtttggc ctccgtctca cactgatcga 900
cgcgctggac accatgtgga tcttggttct gaggaagaa tttgaggaag 950
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050
ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100
atcggctaata gcctgccttc agaacacat ccaagattcc ttactcgat 1150
gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200
cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250
gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
cacatccacg gcctgtcttg gaagaaggat gggctggtgc ccatgttcat 1350
caataccac agtggcctct tccccacct gggcgtattc acgctgggag 1400
ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450
gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500
tgtcagaacg cacctgctgc ggcactccga gccagtaag ctcacctttg 1550
tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600
tgcttctctg cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650
cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750
tacccccagc cgggccgtcg ggacgtggag gtcaagccag cagacaggca 1800
caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgag 1850
tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
tcctggggga gacgtcaag tatctgttct tgctcttctc cgatgacca 2050
aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccacctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150
 ggggtgggcag aggcaccttg ctgggtctgt ggcattttcc aaggggccac 2200
 gtagcaccgg caacgcgcaa gtggcccagg ctctgaactg gctctgggct 2250
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300
 cagtcttggt gtgatgoggg gtgggctggg ccgctggagc ctccgcctgc 2350
 ttcctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400
 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctggaagc 2500
 ctcagatgtc cccaatccaa ggggtctggag gggctgccgt gactccagag 2550
 gcctgagggt ccagggctgg ctctggtgtt tacaagctgg actcagggat 2600
 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650
 tagctcacgg gccctccag tggaatgggt cttttcgggt gagataaaag 2700
 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp	His	Trp	Lys	Ala 110	Leu	Ala	Phe	Arg	Leu 115	Glu	Glu	Glu	Gln	Lys 120
Met	Arg	Pro	Glu	Ile 125	Ala	Gly	Leu	Lys	Pro 130	Ala	Asn	Pro	Pro	Val 135
Leu	Pro	Ala	Pro	Gln 140	Lys	Ala	Asp	Thr	Asp 145	Pro	Glu	Asn	Leu	Pro 150
Glu	Ile	Ser	Ser	Gln 155	Lys	Thr	Gln	Arg	His 160	Ile	Gln	Arg	Gly	Pro 165
Pro	His	Leu	Gln	Ile 170	Arg	Pro	Pro	Ser	Gln 175	Asp	Leu	Lys	Asp	Gly 180
Thr	Gln	Glu	Glu	Ala 185	Thr	Lys	Arg	Gln	Glu 190	Ala	Pro	Val	Asp	Pro 195
Arg	Pro	Glu	Gly	Asp 200	Pro	Gln	Arg	Thr	Val 205	Ile	Ser	Trp	Arg	Gly 210
Ala	Val	Ile	Glu	Pro 215	Glu	Gln	Gly	Thr	Glu 220	Leu	Pro	Ser	Arg	Arg 225
Ala	Glu	Val	Pro	Thr 230	Lys	Pro	Pro	Leu	Pro 235	Pro	Ala	Arg	Thr	Gln 240
Gly	Thr	Pro	Val	His 245	Leu	Asn	Tyr	Arg	Gln 250	Lys	Gly	Val	Ile	Asp 255
Val	Phe	Leu	His	Ala 260	Trp	Lys	Gly	Tyr	Arg 265	Lys	Phe	Ala	Trp	Gly 270
His	Asp	Glu	Leu	Lys 275	Pro	Val	Ser	Arg	Ser 280	Phe	Ser	Glu	Trp	Phe 285
Gly	Leu	Gly	Leu	Thr 290	Leu	Ile	Asp	Ala	Leu 295	Asp	Thr	Met	Trp	Ile 300
Leu	Gly	Leu	Arg	Lys 305	Glu	Phe	Glu	Glu	Ala 310	Arg	Lys	Trp	Val	Ser 315
Lys	Lys	Leu	His	Phe 320	Glu	Lys	Asp	Val	Asp 325	Val	Asn	Leu	Phe	Glu 330
Ser	Thr	Ile	Arg	Ile 335	Leu	Gly	Gly	Leu	Leu 340	Ser	Ala	Tyr	His	Leu 345
Ser	Gly	Asp	Ser	Leu 350	Phe	Leu	Arg	Lys	Ala 355	Glu	Asp	Phe	Gly	Asn 360
Arg	Leu	Met	Pro	Ala 365	Phe	Arg	Thr	Pro	Ser 370	Lys	Ile	Pro	Tyr	Ser 375
Asp	Val	Asn	Ile	Gly 380	Thr	Gly	Val	Ala	His 385	Pro	Pro	Arg	Trp	Thr 390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccc gccgggctgc gagcgctgc 50
cccattgcgc gcgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgttg 200
gcttctctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctoaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcttttctg tctctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggctcc ctagaggccc agcgcagccg 50
cagcggacaa aggagcatgt ccgcgccggg gaaggcccggt cctccggccg 100
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccgcccg 150
ggctccgggg cggcccgtta ggccagtgcg ccgccgctcg ccccgcaggc 200
cccggcccgc agcatggagc caccgcgacg ccggcggggc cgcgcgcagc 250
cgccgctggt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300
ggcggcgggc gcggcgggcg ccgcggcgctg cccgccggct gcaagcacga 350
tgggcggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcagg tcctgcccc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
agacatatct cgaggactca ccaatctggg tcggctaaac ctttcgggga 700
atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacggta cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
 caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950
 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050
 gatgggagaa tagttgaaac cgatgaatcg caaggatatt ttgttgaaaa 1100
 gaacatgatt cacaactgct ccttgattgc aagtgccta accatttcta 1150
 atattcaggc tggatctact ggaaattggg gctgtcatgt ccagaccaa 1200
 cgtgggaata atacgaggac tgtggatatt gtggtattag agagtctgc 1250
 acagtactgt cctccagaga ggtggtaaa caacaaagg gacttcagat 1300
 ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggaac 1350
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400
 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450
 gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500
 atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550
 ttacactgtg gaagcagcca acttttctga caaatggat gttatatttg 1600
 tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650
 aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700
 tgatgaacgt gtccgtgtggc tggcgcagag ggaagctaaa gcctgcagta 1750
 ggattgtgca gtgtcttcag cgcattgcta cctaccggct agccggtgga 1800
 gctcacgttt attcaacata ttcaccaat attgctctgg aagcttatgt 1850
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900
 tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950
 gagggaaacc tggataagca gctgagcttt aagtgaatg tttcaaatac 2000
 attttcgagt ctggcactaa aggtatgtta cattctgcaa tcatttaaga 2050
 ctatttacag ttaaattaga atgctccaaa tgttctgctt cgcaaaataa 2100
 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150
 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
 ggccctagga atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat tttataactg cagtggata aatgcaaata tactattgtt 2300

acatgtgaaa aaatatttatt tgacttaaaa gtttatattat ttgttttttt 2350
 gctcctgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400
 atgagccttt ggcactgcgc ctgccaagcc tagtggagaa gtcaaccctg 2450
 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
 acacaaatat gtcatatatc tttttttaaa aaaagtattt cattgaagca 2550
 agcaaaatga aagcattttt actgattttt aaaattggtg ctttagatat 2600
 atttgactac actgtattga agcaaataga ggaggcacaa ctccagcacc 2650
 ctaatggaac cacatattttt tcacttagct ttctgtgggc atgtgtaatt 2700
 gtattctctg cggttttttaa tctcacagta ctttatttct gtcttgtccc 2750
 tcaataatat cacaaacaat attccagtca ttttaatggc tgcataataa 2800
 ctgatccaac aggtgttagg tgttctgggt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24

<211> 616

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-33

<223> Signal peptide.

<220>

<221> TRANSMEM

<222> 13-40

<223> Transmembrane domain (type II).

<400> 24

Met	Glu	Pro	Pro	Gly	Arg	Arg	Arg	Gly	Arg	Ala	Gln	Pro	Pro	Leu
1				5					10					15

Leu	Leu	Pro	Leu	Ser	Leu	Leu	Ala	Leu	Leu	Ala	Leu	Leu	Gly	Gly
			20					25						30

Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Leu	Pro	Ala	Gly	Cys	Lys	His
			35					40						45

Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu
			50					55						60

Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro
			65					70						75

Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn
			80					85						90

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
				95					100					105	
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	
				110					115					120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
				125					130					135	
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	
				140					145					150	
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
				155					160					165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
				170					175					180	
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
				185					190					195	
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	
				200					205					210	
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	
				215					220					225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	
				230					235					240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	
				245					250					255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
				260					265					270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	
				275					280					285	
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His	
				290					295					300	
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	
				305					310					315	
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	
				320					325					330	
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	
				335					340					345	
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp	
				350					355					360	
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	
				365					370					375	
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro	

	380		385		390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
	590	595	600		
Ala Leu Lys Val	Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr		
	605	610	615		
Ser					

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50
ctgacggcgg ccacagtggc cggcgtagat gtgaagcagc agtgggacca 100
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
aaaaagaaaa cattcgtctt ttgggagAAC agattatctt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttgagca gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
tttggaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500
tgtccagtgc ttaggggtgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600
 atgacgaagc cacgagaaca tcgacctcag aaggactgga ggaaggtgaa 650
 gtggagggag agacgctcct gatcgtcgaa tcc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu
 1 5 10 15
 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
 ctgtcgtctt tgcttcagcc gcagtcgcca ctggctgcct gaggtgctct 50
 tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100
 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250
 ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgtctg tggctagcgt 300
 gggcgccctg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350
 tctgcttctc cgtgacctg atcatcctca tcgtggagct gtgcgggctc 400
 caggcccgcct tccccctgtc ttggcgcaac ttccccatca ccttcgcctg 450

ctatgcggcc ctcttctgcc tctcggcctc catcatctac cccaccacct 500
 atgtccagtt cctgtcccac ggccgttcgc gggaccaogc catcgccgcc 550
 accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600
 gacctggggc cggcccggcg agatcactgg ctatatggcc accgtaccgc 650
 ggctgctgaa ggtgctggag accttcgttg cctgcatcat cttcgcgttc 700
 atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtgcgt 750
 ggcgggtgtac gccatctgct tcatcctagc ggccatcgcc atcctgctga 800
 acctggggga gtgcaccaac gtgctacca tcccttccc cagcttctctg 850
 tcggggctgg ccttgctgtc tgcctcctc tatgccaccg cccttggtct 900
 ctggccctc taccagttcg atgagaagta tggcggccag cctcggcgct 950
 cgagagatgt aagctgcagc cgcagccatg cctactacgt gtgtgcctgg 1000
 gaccgccgac tggctgtggc catcctgacg gccatcaacc tactggcgta 1050
 tgtggctgac ctgggtgact ctgccacct ggtttttgc aagggtctaag 1100
 actctcccaa gaggtcccg ttcctctcc aacctcttg ttcttcttg 1150
 ccgagttttc tttatggagt acttctttcc tccgcctttc ctctgttttc 1200
 ctcttctgt ctccctccc tccaccttt ttctttcctt cccaattcct 1250
 tgcactctaa ccagttcttg gatgcatctt ctctctccc ttctctcttg 1300
 ctgtttcctt cctgtgttgt tttgttgccc acatcctgtt ttcaccttg 1350
 agctgtttct cttttcttt tctttcttt ttttttttt ttttaagacg 1400
 gattctcact ctgtggccca ggctggagtg cagtgggtgc atctcagctc 1450
 actgcaaccc ccgcctcctg ggttcaagcg attctcctcc cccagcctcc 1500
 caagtagctg ggaggacagg tgtgagctgc cgcaccacgc ctgtttctct 1550
 ttttccactc ttcttttttc tcactcttt tctgggttgc ctgtcggctt 1600
 tcttatctgc ctgttttgca agcacctct cctgtgtcct tgggagccct 1650
 gagacttctt tctctccttg cctccacca cctccaaagg tgctgagctc 1700
 acatccacac cccttgacgc cgtccatgcc acagccccc aaggggcccc 1750
 attgccaaag catgcctgcc caccctcgct gtgccttagt cagtgtgtac 1800
 gtgtgtgtgt gtgtgtgttt ggggggtggg ggggtggtag ctggggattg 1850
 ggccctcttt ctccagtg aggaaggtgt gcagtgtact tccctttta 1900

attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950
 gcgggaggca ttaagcacccg accctgggtc cctaggcccc gcctggcact 2000
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050
 ccactgccta gaggccatct taaaggaagc aggggctgga tgcctttcat 2100
 cccaactatt ctctgtggta tgaaaaag 2128

<210> 31

<211> 322

<212> PRT

<213> Homo sapiens

<400> 31

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Thr	1	5	10	15
Ser	Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg	20	25	30	
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	35	40	45	
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	50	55	60	
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	65	70	75	
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	80	85	90	
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	95	100	105	
Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	110	115	120	
Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	125	130	135	
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	140	145	150	
Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	155	160	165	
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu	170	175	180	
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	185	190	195	
Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr	200	205	210	

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
				305					310					315	
His	Leu	Val	Phe	Val	Lys	Val									
				320											

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

```

gaacgtgccca ccatgcccag ctaatttttg tatttttagt agagacgggg 50
tttcaccatg ttggccaggc tgggtcttgaa ctcgtgacct catgatccgc 100
tcacctcggc ctcccaaagt gctgggatta caggcatgag ccactgacgc 150
ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200
taaacattgg gcactacagt gacaaaaaca gactgaattc cccaagagcc 250
aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300
ttattactca ctatgactaa gggtcacaaa tgggggtacgt tgatggagag 350
tgatttggtta agagactaca gagggaggac agactaccaa gagggggggc 400
aggaaagctc ctctgacgag gtgggtatttc agcccaaact ggaagaatga 450
gaaagagcta gccagccatc agaatagtc agagagatg gggagcacta 500
cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550
ggggaacacc acttctgccc acctgggcag gaggcattga gggcttgaga 600
aagggcaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650
gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700

```


ggctcattag gtgtttatatt tgttctatatt aagaatttgt tttattaaat 3650

taatataaaa atctttgttaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
1 5 10 15

Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
20 25 30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245					250						255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
				335										

```

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
      tgtcctttgt cccagacttc tgtcc 25

```

```

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
      ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

```

```

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

```


ttccactcaa tgagggtgagc cactc 25

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 37
 ggcgagccct aactatccag gag 23

<210> 38
 <211> 39
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-39
 <223> Synthetic construct.

<400> 38
 ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 39
 ctgctgcaaa gcgagcctct tg 22

<210> 40
 <211> 2084
 <212> DNA
 <213> Homo sapiens

<400> 40
 ggttcctggg cgctctgtta cacaagcaag atacagccag cccaccta 50
 ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100
 ccattctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150
 tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200
 tactagccat tgtgagcttc agttttcttca tctgcaaaat gggcataata 250
 caatctattc ttgccacatc aagggtattgt tattccttta aaaaaaacc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
caacgttgtt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
atataaccac ctcaaacttc aaggcgagtc attcccctcc tttgaatcta 550
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700
gatgaagatc ttttgcccat ctcagcacat cccaatgcta cacctgctct 750
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
ccatctgtga ccccttgat agtggaacca agtggaatggc ttaccacaaa 900
cagtgatagc ttacttgggt ttaccctta tcaagaaaaa acaactctac 950
agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050
aggtgctatt ctgggtgtct cattgttac tcttgtgggc tacttgttgt 1100
gtggaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150
agaaatgaac cagtctgcg attagacaat gcacoggaac cttatgatgt 1200
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250
tgccagaaaag tgaagaaaat gcacgtgatg gcatttctat ggatgacata 1300
cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350
gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450
aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggttttc 1500
tttcttacia tttttggcca tcttgaggca tttactaagt agccttaatt 1550
tgtattttag tagtattttc ttagtagaaa atatttgtgg aatcagataa 1600
aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650
attattccac caaaaaatc taaaacaatg aagatgactc tttactgctc 1700
tgctgaagc ctagtacca taattcaaga ttgcattttc ttaaatgaaa 1750

attgaaaggg tgcttttttaa agaaaatttg acttaaagct aaaaagagga 1800
catagcccag agtttctgtt attgggaaat tgaggcaata gaaatgacag 1850
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000
aagggttttg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41

Met	Leu	Ala	Leu	Ala	Lys	Ile	Leu	Leu	Ile	Ser	Thr	Leu	Phe	Tyr
1				5					10					15
Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
				20					25					30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
				35					40					45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
				50					55					60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
				65					70					75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
				80					85					90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
				95					100					105
Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val
				110					115					120
Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser
				125					130					135
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr
				140					145					150
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser
				155					160					165
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val
				170					175					180
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser
				185					190					195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330
Arg	Thr	Ser	Val											

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

```

aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50
gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100
cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
tgccaccagc gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
tacaagtact tcatgcccac gagcaccatt taccgtggag agatgtgctt 350
ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
atcattgatg tgctgtccc cagttttctt gatagtgacc ctgcagcaat 500
tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

```


50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccagggtgcc cccactctcg ctccattcgg 100
 cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150
 gtttcggcgg cagccccag cctcctcatc cttctgttgc tgetgctggg 200
 gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggctcctcc 300
 ccgagcctcc cgccaccctg gaccccggcc ctacgcccc catcgatggg 350
 gccccagccc acaaccctgg ggggcccatc accccccacc aaattcctgg 400
 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450
 ggctccctgg ctttctgtct gatgttcacg gtctgtgcgg cggtcacac 500
 ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
 ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
 cccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750
 ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
 agtcaggga catggggtcc cagtggagac accagaggcg caggaggagc 850
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
 gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950
 tcccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000
 agtcctcccg ggctgccagc cctgaactgc gggcccccaa gtggtcacct 1050
 ccccggtgat gaaaaggcct tcagccctga ctgcttctcg aactccctc 1100
 cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150
 cagaaatgct ggtccccggt gcccggagg aatcttacca agtgccatca 1200
 tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
 aatactgctc ttaattttcc tgaagggtgg ccctgtttc tagttggtcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550
 gatcagggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
 ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatatcc 1750
 gtcagtcctc gacagggagc ctgggctccg tcttgcttta gggaggctct 1800
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccagggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	20	25	30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	35	40	45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	50	55	60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly	65	70	75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	80	85	90	
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	95	100	105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	110	115	120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	125	130	135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	140	145	150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	155	160	165	

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
				245					250					255	
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
				260					265					270	
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			
				275					280						

<210> 51

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

```

gtggactctg agaagccag gcagttgagg acaggagaga gaaggctgca 50
gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
cctggcctgc ctctgctgg cctctgcct gggcagtggg gaggctggcc 250
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
caaagaggcc ggaggggcag ctggctctaa agtcagtgag gcccttggcc 400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

```


1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

				50						55					60
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr	
				65					70					75	
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly	
				80					85					90	
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala	
				95					100					105	
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val	
				110					115					120	
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val	
				125					130					135	
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile	
				140					145					150	
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro	
				155					160					165	
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser	
				170					175					180	
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln	
				185					190					195	
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly	
				200					205					210	
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln	
				215					220					225	
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly	
				230					235					240	
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser	
				245					250					255	
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly	
				260					265					270	
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser	
				275					280					285	
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser	
				290					295					300	
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly	
				305					310					315	
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His	
				320					325					330	
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly	
				335					340					345	

Glu Ser Gly Ile	Gln Gly Phe Arg Gly	Gln Gly Val Ser Ser	Asn
350	355		360
Met Arg Glu Ile	Ser Lys Glu Gly Asn	Arg Leu Leu Gly Gly	Ser
365	370		375
Gly Asp Asn Tyr	Arg Gly Gln Gly Ser	Ser Trp Gly Ser Gly	Gly
380	385		390
Gly Asp Ala Val	Gly Gly Val Asn Thr	Val Asn Ser Glu Thr	Ser
395	400		405
Pro Gly Met Phe	Asn Phe Asp Thr Phe	Trp Lys Asn Phe Lys	Ser
410	415		420
Lys Leu Gly Phe	Ile Asn Trp Asp Ala	Ile Asn Lys Asp Gln	Arg
425	430		435
Ser Ser Arg Ile	Pro		
440			

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaccggtccc tccggtcctg gatgtgcgga ctctgctgca gcgagggctg 50
 caggcccgcc gggcggtgct caccgtgccc tggctggtgg agtttctctc 100
 ctttgcctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
 ctctcctgct ggcctgcac cggagcttgg tgttgctgca ggagagttag 200
 gggaagatgt gtttcctgaa caagctgctg ctacttgctg tcctgggctg 250
 gcttttccag attccacag tccctgagga cttgttcttt ctggaagagg 300
 gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350
 gacaatgctg ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
 catcggagag ctccggaac tgctcgcttc gtgggtgtca ggcagtagtg 450
 gacggagtgg gggcttcatg aggaaaatca cccccaccac taccaccagc 500
 ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550
 ccaggccttt ttccacaacc agccgccctc cttgcgcggg accgtagagt 600
 tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650
 ctggtggcag atctggtgcg ccaggcagag tcaacttctcc aagagcagct 700
 ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750
 tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800

gagtttctgtc aaaggaagag ccctggggct gtgcggggcgc tgcttccaga 850
 ggagacccccg gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900
 ttgcaacaga gaaagcctgt gcttggctgt cagccaacat cacagcactg 950
 atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000
 tcctgaacct gctgcccggg gggagcggag gggctgctcc cgcgcctgac 1050
 gtgctctcct tggccgtggg gccacgggac cctgacgagg gagtctcccc 1100
 agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150
 gccagttcct gtgccacct gctgagcagc atctggcaaa gtgctctgtg 1200
 gagttagctt ccctcctcgt tgcagatcaa attcctatcc tagggccccc 1250
 ggcacagtac aggctggaga gagggcaggc tcgaaggctt ctgcacatgc 1300
 tgctttcctt gtggaaggaa gactttcagg ggccggttcc gctgcagctg 1350
 ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400
 gtgggacttg ctgctattct tgctacggga gctgggtggag aagggtctga 1450
 tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggcccag 1500
 tggccagggg actttgctga agaattagca acactgtcta atctgtttct 1550
 agccgagccc cacctgccag aaccccagct aagagcctgt gagttgggtgc 1600
 agccaaaccg gggcactgtg ctggcccaga gctagggctg agaagtggcc 1650
 ctgccttggg cattgcacca gaaccctgga ccccccgcctc acgaggaggc 1700
 ccaagtgcc aatgcagacc ctactgggtt ggggtgtagc tgggtctaca 1750
 gtcagacttc ctgctctaag ggtgtcaact cctggcatcc caccacgcga 1800
 atcctagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850
 cagagatgcc agtcctggag tagaagaggt ggtgtttggt tatctcttgg 1900
 atactaaatg aaatgaggtg tgtgggcttg tcaacacaga attcaagcct 1950
 catttgctat ccagcatct cttaaaactt tgtagtcttg gaattcatga 2000
 cagaggcaaa tgactcctgc ttaacttatg aagaaagtta aaacatgaat 2050
 cttgggagtc tacattttct tatcaccagg agctggactg ccatctcctt 2100
 ataaatgcct aacacaggcc gggctctggtg gctcatgcct gtaatcccag 2150
 cactttgaga ggcctgaggt cggcggactg cctgagggtca ggaattcaag 2200
 accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250

ttattagctg ggcatggtgg tgtgtgcctg taatcccagc tactcaggag 2300
 gatgaggcag gagacctgct tgaacctgga ggtggagggt gcagtgagcc 2350
 gaggtcgcac cactgcactc cagtctgggt aacagagcga gactttctag 2400
 aaaaagccta acaaacagat aaggtaggac tcaaccaact gaaacctgac 2450
 tttcccctg taccttcagc cctgtgcag gtagtaacct cttgagacct 2500
 ctccctgacc agggaccaag cacagggcat ttagagcttt ttagaataaa 2550
 ctggttttct ttaaaaaaaa aaaaaaaaaa agggcgggccg cccttttttt 2600
 tttttttttt tttttttttt tttttttttt tttttttttt taaaaagggc 2650
 ttttattaaa attctcccca cacgatggct cctgcaatct gccacagctc 2700
 tggggcgtgt cctgtaggga aaggccctgt tttccctgag gcggggctgg 2750
 gcttgtccat ggggtccgcg agctggccgt gcttggcgcc ctggcgtgtg 2800
 tctagctgct tcttgccggg cacagagctg cggggctctg gggcaccggg 2850
 agctaagagc aggcctctgt gcaggggtgg aggcctgtct cttaacgcac 2900
 accctgaggt gtcctgaga tgctgggtcc accctgagtg gcacggggag 2950
 cagctgtggc cgggtctcct tcytaggcca gtcctgggga aactaagctc 3000
 gggcccttct ttgcaaagac cgaggatggg gtgggtgtgg gggactcatg 3050
 gggaatggcc tgaggagcta cgtgtgaaga gggcgccggg ttgttggtctg 3100
 cagcggcctg gagcgccctc ctccctgagc tcagtttccc tttccgtcta 3150
 atgaagaaca tgccgtctcg gtgtctcagg gctattagga cttgccctca 3200
 ggaagtggcc ttggacgagc gtcattgtat tttcacaact gtccctgcgac 3250
 gttggcctgg gcacgtcatg gaatggccca tgtccctctg ctgcgtggac 3300
 gtcgcggtcg ggagtgcgca gccagaggcg gggccagacg tgcgcctggg 3350
 ggtgagggga ggcgccccg gagggcctca caggaagttg ggctcccga 3400
 ccaccaggca gggcgggctc ccgcgcgcgc cgccgccacc accgtccagg 3450
 ggccggtaga caaagtggaa gtgcgcgttg ggctcgctgc gcagcaggta 3500
 gcccttgatg cagtgcggca gcgcgtcgtc cgccagctgg aagcagcgcc 3550
 cgtccaccag cacgaacagc cgggtgcgct 3580

<210> 54
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 54

Met	Cys	Phe	Leu	Asn	Lys	Leu	Leu	Leu	Leu	Ala	Val	Leu	Gly	Trp
1				5					10					15
Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu
				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
				275					280					

<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
tcccttgaca ggtctggtgg ctggttcggg gtctactgaa ggctgtcttg 50
atcaggaaac tgaagactct ctgcttttgc cacagcagtt cctgcagctt 100
ccttgagggtg tgaaccaca tccctgcccc cagggccacc tgcaggacgc 150
cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200
gcagcgggtca gcagtgttcg tgatcctctt tgcctcatc accatcctca 250
tcctctacag ctccaacagt gccaatgagg tcttccatta cggctccctg 300
cggggccgta gccgccgacc tgtcaacctc aagaagtgga gcatcactga 350
cggctatgtc cccattctcg gcaacaagac actgccctct cggtgccacc 400
agtgtgtgat tgtcagcagc tccagccacc tgctgggcac caagctgggc 450
cctgagatcg agcgggctga gtgtacaatc cgcataatg atgcacccac 500
cactggctac tcagctgatg tgggcaacaa gaccacctac cgcgtcgtgg 550
cccattccag tgtgttccgc gtgctgagga ggcccagga gtttgtcaac 600
cggacccttg aaaccgtgtt catcttctgg gggccccga gcaagatgca 650
gaagccccag ggcagcctcg tgcgtgtgat ccagcgagcg ggcctggtgt 700
tccccaatat ggaagcatat gccgtctctc ccggccgcat gcggcaattt 750
gacgacctct tccggggtga gacgggcaag gacagggaga agtctcattc 800
gtggttgagc acaggctggt ttaccatggt gatcgcggtg gagttgtgtg 850
accacgtgca tgtctatggc atgggtcccc ccaactactg cagccagcgg 900
ccccgcctcc agcgcagcct ctaccactac tacgagccca aggggccgga 950
cgaatgtgtc acctacatcc agaatgagca cagtcgcaag ggcaaccacc 1000
accgcttcat caccgagaaa agggctcttct catcgtgggc ccagctgtat 1050
ggcatcacct tctcccaccc ctcttgagcc taggccaccc agcctgtggg 1100
acctcaggag ggtcagagga gaagcagcct ccgccagcc gctaggccag 1150
ggaccatctt ctggccaatc aaggcttgct ggagtgtctc ccagccaatc 1200
agggccttga ggaggatgta tcctccagcc aatcagggcc tggggaatct 1250
gttggcgaat cagggatttg ggagtctatg tggttaatca ggggtgtctt 1300

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400

tcttgtgcag tcaggggtctg cgcacagtca atcagggtag aggggggtatt 1350
tctgagtcaa tctgaggcta aggacatgtc ctttcccatg aggccttggt 1400
tcagagcccc aggaatggac cccccaatca ctccccactc tgctgggata 1450
atgggggtcct gtcccaagga gctgggaact tgggtgttgcc ccctcaattt 1500
ccagcaccag aaagagagat tgtgtggggg tagaagctgt ctggaggccc 1550
ggccagagaa tttgtggggg tgtggagggt gtggggggcgg tggggaggtc 1600
ccagagggtg gaggctggca tccaggctct ggctctgccc tgagaccttg 1650
gacaaaccct tccccctctc tgggcaccct tctgccaca ccagtttcca 1700
gtgcgagtc tgagaccctt tccacctccc ctacaagtgc cctcgggtct 1750
gtcctccccg tctggaccct ccagccact atcccttgct ggaaggctca 1800
gctctttggg gggctctggg tgacctcccc acctcctgga aaactttagg 1850
gtatTTTTgc gaaactcct tcaggggttg gggactctga aggaaacggg 1900
acaaaaccct aagctgtttt cttagccct cagccagctg ccattagctt 1950
ggctcttaaa gggccaggcc tccttttctg ccctctagca gggaggtttt 2000
ccaactgttg gaggcgcctt tggggctgcc cctttgtctg gagtcactgg 2050
gggcttccga gggctcctc cgaccctctg tegtctggg atggctgtcg 2100
ggagctgtat cacctgggtt ctgtcccctg gctctgtatc aggcacttta 2150
ttaaagctgg gcctcagtgg ggtgtgtttg tctcctgctc ttctggagcc 2200
tggaaggaaa gggcttcagg aggaggctgt gaggctggag ggaccagatg 2250
gaggaggcca gcagctagcc attgcacact ggggtgatgg gtggggggcgg 2300
tgactgcccc agacttggtt ttgtaatgat ttgtacagga ataaacacac 2350
ctacgtccg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2400

a 2401

<210> 56
<211> 299
<212> PRT
<213> Homo sapiens

<400> 56
Met Ser Ser Asn Lys Glu Gln Arg Ser Ala Val Phe Val Ile Leu
1 5 10 15
Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser Ser Asn Ser Ala
20 25 30

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg	
				35					40					45	
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro	
				50					55					60	
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val	
				65					70					75	
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro	
				80					85					90	
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	
				95					100					105	
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg	
				110					115					120	
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln	
				125					130					135	
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly	
				140					145					150	
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val	
				155					160					165	
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala	
				170					175					180	
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly	
				185					190					195	
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr	
				200					205					210	
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val	
				215					220					225	
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro	
				230					235					240	
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro	
				245					250					255	
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly	
				260					265					270	
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp	
				275					280					285	
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr		
				290					295						

<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57

gtttctcata gttggcgtct tctaaaggaa aaacactaaa atgaggaact 50
cagcggaccg ggagcgacgc agcttgaggg aagcatccct agctgttggc 100
gcagaggggc gaggctgaag ccgagtggcc cgaggtgtct gaggggctgg 150
ggcaaagggtg aaagagtttc agaacaagct tcctggaacc catgacccat 200
gaagtcttgt cgacatttat accgtctgag ggtagcagct cgaaactaga 250
agaagtggag tgttgccagg gacggcagta tctctttgtg tgaccctggc 300
ggcctatggg acgttggctt cagacctttg tgataacca tgctgcgtgg 350
gacgatgacg gcgtggagag gaatgaggcc tgaggtcaca ctggcttgcc 400
tcctcctagc cacagcaggc tgctttgctg acttgaacga ggtccctcag 450
gtcaccgtcc agcctgcgtc caccgtccag aagcccggag gcactgtgat 500
cttgggctgc gtggtggaac ctccaaggat gaatgtaacc tggcgccctga 550
atggaaagga gctgaatggc tcggatgatg ctctgggtgt cctcatcacc 600
cacgggaccc tcgtcatcac tgcccttaac aaccacactg tgggacggta 650
ccagtgtgtg gcccggatgc ctgcgggggc tgtggccagc gtgccagcca 700
ctgtgacact agccaatctc caggacttca agttagatgt gcagcacgtg 750
attgaagtgg atgagggaaa cacagcagtc attgcctgcc acctgcctga 800
gagccacccc aaagcccagg tccggtacag cgtcaaacia gagtggctgg 850
aggcctccag aggtaactac ctgatcatgc cctcagggaa cctccagatt 900
gtgaatgcca gccaggagga cgagggcagc tacaagtgtg cagcctacia 950
cccagtgacc caggaagtga aaacctccgg ctccagcgac aggctacgtg 1000
tgcgccgctc caccgctgag gctgcccga tcatctaccc cccagaggcc 1050
caaaccatca tcgtcaccaa aggccagagt ctcatctctg agtgtgtggc 1100
cagtggaatc ccacccccac gggtcacctg ggccaaggat ggggtccagt 1150
tcaccggcta caacaagacg cgcttcctgc tgagcaacct cctcatcgac 1200
accaccagcg aggaggactc aggcacctac cgctgcatgg ccgacaatgg 1250
ggttgggcag cccggggcag cggtcatcct ctacaatgtc caggtgtttg 1300
aaccctctga ggtcaccatg gagctatccc agctggatcat cccctggggc 1350
cagagtgcca agcttacctg tgaggtgctg gggaaccccc cgccctccgt 1400
gctgtggctg aggaatgctg tgccctcat ctccagccag cgcctccggc 1450

tctcccgag ggccctgcgc gtgctcagca tggggcctga ggacgaaggc 1500
 gtctaccagt gcatggccga gaacgaggtt gggagcgccc atgccgtagt 1550
 ccagctgcgg acctccaggc caagcataac cccaaggcta tggcaggatg 1600
 ctgagctggc tactggcaca cctcctgtat caccctccaa actcggcaac 1650
 cctgagcaga tgctgagggg gcaaccggcg ctccccagac cccaacgtc 1700
 agtggggcct gcttccccga agtgtccagg agagaagggg cagggggctc 1750
 ccgccgaggc tcccatcatc ctgagctcgc ccgcacctc caagacagac 1800
 tcatatgaac tgggtgtggcg gcctcggcat gagggcagtg gccgggagcc 1850
 aatcctctac tatgtgtgta aacaccgcaa gcaggtcaca aattcctctg 1900
 acgattggac catctctggc attccagcca accagcaccg cctgaccctc 1950
 accgacttg accccgggag cttgtatgaa gtggagatgg cagcttaca 2000
 ctgtgcggga gagggccaga cagccatggt caccttcga actggacggc 2050
 ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100
 gaccctggag ccagtcccca gagcagcagc cagccagacc acggccgcct 2150
 ctcccccca gaagctcccg acaggccac catctccacg gcctccgaga 2200
 cctcagtgtg cgtgacctgg attccccgtg ggaatgggtg gttcccaatc 2250
 cagtccttcc gtgtggagta caagaagcta aagaaagtgg gagactggat 2300
 tctggccacc agcgccatcc cccatcgcg gctgtccgtg gagatcacgg 2350
 gcctagagaa aggcacctcc tacaagtttc gagtccgggc tctgaacatg 2400
 ctgggggaga gcgagcccag cgcacctct cggccctacg tgggtgcggg 2450
 ctacagcggg cgcggtgtac agaggcccgt ggaggtcct tatatcacct 2500
 tcacggatgc ggtcaatgag accaccatca tgetcaagt gatgtacatc 2550
 ccagcaagta acaacaacac ccaatccat ggcttttata tctattatcg 2600
 acccacagac agtgacaatg atagtgacta caagaaggat atggtggaag 2650
 gggacaagta ctggcactcc atcagccacc tgcagccaga gacctctac 2700
 gacattaaga tgcagtgctt caatgaagga ggggagagcg agttcagcaa 2750
 cgtgatgatc tgtgagacca aagctcgga gtcttctggc cagcctgggtc 2800
 gactgccacc cccaactctg gccccaccac agccgccct tctgaaacc 2850
 atagagcggc cgggtgggac tggggccatg gtggctcgt ccagcgacct 2900

gccctatctg attgtcgggg tcgtcctggg ctccatcggt ctcatcatcg 2950
 tcaccttcat ccccttctgc ttgtggaggg cctgggtctaa gcaaaaacat 3000
 acaacagacc tgggttttcc tcgaagtgcc cttccaccct cctgcccgtg 3050
 tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100
 cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150
 aataggggct gccctcggc tgcatgggc taccgggca tgaagcccca 3200
 gcagcactgc ccaggcgagc ttcagcagca gagtgacacc agcagcctgc 3250
 tgaggcagac ccatcttggc aatggatatg acccccaaag tcaccagatc 3300
 acgaggggtc ccaagtctag cccggacgag ggctctttct tatacacact 3350
 gcccgacgac tccactcacc agctgctgca gcccacac gactgctgcc 3400
 aacgccagga gcagcctgct gctgtgggcc agtcaggggt gaggagagcc 3450
 cccgacagtc ctgtcctgga agcagtgtgg gaccctccat ttcactcagg 3500
 gcccccatgc tgcttgggcc ttgtgccagt tgaagaggtg gacagtctg 3550
 actcctgcca agtgagtgga ggagactggt gtcccagca cccgtaggg 3600
 gcctacgtag gacaggaacc tggaatgcag ctctccccgg ggccactggt 3650
 gcgtgtgtct tttgaaacac cacctctcac aatttaggca gaagctgata 3700
 tcccagaaag actatatatt gttttttttt taaaaaaaaa agaagaaaaa 3750
 agagacagag aaaattggta tttatttttc tattatagcc atatttatat 3800
 atttatgcac ttgtaaataa atgtatatgt tttataattc tggagagaca 3850
 taaggagtcc taccggttga ggttgagag ggaaaataaa gaagctgcca 3900
 cctaacagga gtcaccagg aaagcaccgc acaggctggc gcgggacaga 3950
 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000
 agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050
 tgagggaaca gcaaggggca cggatcaca gcctggagac acccacacag 4100
 atggctggat ccggtgctac gggaaacatt ttcctaagat gcccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200
 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250
 aataaatggt tagtcttccc tgtaaaa 4277

<210> 58
 <211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu	
1				5					10					15	
Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala	
				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu	275	280	285
Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met	290	295	300
Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr	305	310	315
Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser	320	325	330
Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu	335	340	345
Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala	350	355	360
Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala	365	370	375
Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	380	385	390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	395	400	405
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	410	415	420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	425	430	435
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	440	445	450
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	455	460	465
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	470	475	480
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	485	490	495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	500	505	510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	515	520	525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	530	535	540
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	545	550	555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg			

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln 575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp 590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile 605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg 620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys 635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile 650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly 665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu 680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr 695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr 710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met 725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr 740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys 755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His 770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn 785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr 800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro 815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg 830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro 845	850	855

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
				950					955					960	
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	
				965					970					975	
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	
				980					985					990	
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	
				995					1000					1005	
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
				1010					1015					1020	
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	
				1025					1030					1035	
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	
				1040					1045					1050	
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
				1055					1060					1065	
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	
				1070					1075					1080	
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	
				1085					1090					1095	
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	
				1100					1105					1110	
Pro	Pro	Leu	Thr	Ile											
				1115											

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccocaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccat 50
cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100
cacggggcgc gagggttccc gcgcgtcag ccggcggtat ctgcggcgtc 150
tgctgtcct gctactgtg ctgctgtgc ggcagcccgt aaccgcgcg 200
gagaccagc cgggcgcccc cagagccctc tccacgtgg gctccccag 250
cctcttcacc acgcggggtg tccccagcgc cctcactacc ccaggcctca 300
ctacgccagg caccocaaa accctggacc ttccggggtcg cgcgcaggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
 cctgagacag cggtacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
 tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
 gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
 cgtgcgcctc gccctggagc agattgacct cattcacgc atgtgtgcct 600
 cctactctga actcgagctt gtgacctcag ctgaaggtct gaacagctct 650
 caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
 cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
 cacttacctt cacotgcagt acaccatggg cagagagttc caccaagttc 800
 agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850
 agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
 catcggacac cttgataaga agggctctgg aagtgtctca ggctcctgtg 950
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtg 1050
 cactgtccat ggggggtgctg cagtgaacc tgcttgctaa cgtgtccact 1100
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150
 cgggattggg ggaaattatg acgggactgg ccggttcctt caggggctgg 1200
 aggatgtgtc cacataccca gtcctgatag aggagtgtct gagtctasc 1250
 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
 tggagggtga gtttccatat gggcaactga gcacatcctg ccactcccac 1400
 ctctgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgctgacaca gtcgggtccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63

<211> 487

<212> PRT

<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	1	5	10	15
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

	260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro	275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu	290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly	305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu	320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg	335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp	350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu	380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val	410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser	425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val	440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala	455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro	470	475	480
Thr Phe Thr Gln Trp Leu Cys	485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttagc acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50

aacaccacaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100

ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150

cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200

tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250

tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300

gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350

agtgcaggtg cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400

atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450

gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500

acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550

tccctcgggg gaccccagc aaacacagtc ctggagcgtg tggaaggtgc 600

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala
				140					145					150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155					160					165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
				170					175					180
Met	Leu	Ser												

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
 agttcatagg gtcctgggtc cccgaaccag gaagggttga gggaacacaa 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggctctccc 150
 tccctttgca ttccacccc tccgggcttt gcgtcttctt ggggaccccc 200
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550
 gcatgtgctg cccagttacc cgctgcaata atggcatctg tatcccagtt 600
 actgaaagca tcttaacccc tcacatccc gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800
tcatttctgg accaaaaatct gcaaaccagt gctccatcag ggggaagtct 850
gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100
gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350
ttatacaaat aacctacatg ccagatttct attcaacgtt agagttaaac 1400
aaaatactcc tagaataaact tgttatacaa taggttctaa aaataaaatt 1450
gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggg 1550
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
ccacaaatac ttttttttca aaattttagt tttacctgta attaataaga 1700
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750
atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800
aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850
ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900
gctaacagag agatcattat ttcttaaaga ttggcataa cctatatttt 1950
gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150
 tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200
 tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250
 tgctgagatc ctcaaataat ctcaatttca ggaggtttca caaaatgtac 2300
 tcctgaagta gacagagtag tgaggtttca ttgccctcta taagcttctg 2350
 actagccaat ggcacatcc aattttcttc ccaaacctct gcagcatctg 2400
 ctttattgcc aaagggttag ttctggtttt ctgcagccat tgcggttaaa 2450
 aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500
 accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550
 aactcagttc taaatacttt gtctggagca caaaacaata aaaggttatc 2600
 ttatagtcgt gactttaaac ttttgtagac cacaattcac tttttagttt 2650
 tcttttactt aaatcccatc tgcagtttca aattttaagtt ctcccagtag 2700
 agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
 tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
 caaaaattat aaactagtcc atccaagaac caaagtgtgt ataaacaggt 2850
 tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900
 atataacaat tattatatatt acaatttggt ttctgcaata tttttcttat 2950
 gtccaccctt ttaaaaaatta ttatttgaag taatttattt acaggaaatg 3000
 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
 gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
 taagataaaa tctattaaat ttttctcttc taaaaactga aaaaaaaaaa 3150
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
1				5					10					15
Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	50	55	60
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	65	70	75
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	80	85	90
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	95	100	105
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	110	115	120
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	125	130	135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	140	145	150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	155	160	165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	170	175	180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	185	190	195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	200	205	210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	215	220	225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	230	235	240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	245	250	255
Cys Gln Lys Ile																	

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

tctcaatctg ctgacctcgt gatccgcctg accttgtaat ccacctacct 50

tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100

acatcacgtt tttaaaaatt gattttctca aattcatggc aaatatttcc 150

cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
atatttttagt aattcatatg ttttagatta taggttttaa catacttgtg 300
aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
ctcaagcccc caacatccca gtccctcagtc ctcagtcctc ttgacttcaa 600
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
agcaccagag ccaggcagtc actgttcctc ctccctgggtt ggagtccttt 700
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
tgtgaacaag cttttgcagc ttccagcac gaccattgaa aatatctctg 800
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
atacccccag cttctaagat ccagcttct gcagtggaaa tgcctgggtc 900
agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950
cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000
aatcagattc ccatcagctt gtattogaag tctttaagt agcctttgaa 1050
tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100
ccgtcattac ctccctcagc ctgacaagct catcactgaa ttctgctagt 1150
ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200
cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
tgaatggaca tgggtggtgt cgaagtcagc agacactaga cagtaagtat 1300
agcagcaagc tactcttgtc atggctggtg ccaaccaaac agaggaagag 1350
gatagctcac gtgatgtgga aaacaccagt tggatcaatgg ctcatctgtt 1400
aaaaagcagc ccttttgctt ttttgtttt ggaccaggtg ttggctgtgg 1450
tgttattaga aatgtcttaa ccacagcaag aaggaggtgg tggctctcata 1500
ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550
tttaaagatg cttgggccag gcggggtggc tgatgccat aatcccagtg 1600
ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
1 5 10 15
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
245 250 255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
305 310 315

Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
320 325 330

Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
350 355 360

Leu Ile Arg

<210> 73

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-26

<223> Synthetic construct.

<400> 73

aattcatggc aaatatttcc cttccc 26

<210> 74

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 74

tggtaaactg gcccaaactc gg 22

<210> 75

<211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac cgcgccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50
ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100
tgactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagggt 200
caccgacggc cccccggcca cccccgcta ctgggacggc gagaaggagg 250
tgctggcggg ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtgggtgca 350
ctgggaccgg cagccgcccg ggggtcccga cgaccgcgcg gaccgcctgc 400
tgacactcta cgcgtcgggc gagcgcgcgc cctacgggac cctttttctg 450
cgcgaccgcg tggctgtggg cgcggtatgcc tttagcgcgc gtgacttctc 500
actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550
acctgcacca ccattactgt ggcttgcaag aacgcgcgtt cttccacctg 600
acggtcgccc aaccccacgc ggagccgccc ccccggggct ctccgggcaa 650
cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750
cagcagctgg gctacgtgct ggccaogctg ctgctcttca tctgctact 800
ggtcactgtc ctcttgcccg cccgcaggcg ccgcggaggc tacgaatact 850
cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900
ttcgctgtgg ctgcagggga ccagatgctt tacaggagtg aggacatcca 950
gctagattac aaaaacaaca tctgaagga gagggcggag ctggcccaca 1000
gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

Ala Arg Gly Ala	Pro Ala Leu Leu Thr	Cys Val Asn Arg Gly His	
	80	85	90
Val Trp Thr Asp	Arg His Val Glu Glu	Ala Gln Gln Val Val His	
	95	100	105
Trp Asp Arg Gln	Pro Pro Gly Val Pro	His Asp Arg Ala Asp Arg	
	110	115	120
Leu Leu Asp Leu	Tyr Ala Ser Gly Glu	Arg Arg Ala Tyr Gly Pro	
	125	130	135
Leu Phe Leu Arg	Asp Arg Val Ala Val	Gly Ala Asp Ala Phe Glu	
	140	145	150
Arg Gly Asp Phe	Ser Leu Arg Ile Glu	Pro Leu Glu Val Ala Asp	
	155	160	165
Glu Gly Thr Tyr	Ser Cys His Leu His	His His Tyr Cys Gly Leu	
	170	175	180
His Glu Arg Arg	Val Phe His Leu Thr	Val Ala Glu Pro His Ala	
	185	190	195
Glu Pro Pro Pro	Arg Gly Ser Pro Gly	Asn Gly Ser Ser His Ser	
	200	205	210
Gly Ala Pro Gly	Pro Asp Pro Thr Leu	Ala Arg Gly His Asn Val	
	215	220	225
Ile Asn Val Ile	Val Pro Glu Ser Arg	Ala His Phe Phe Gln Gln	
	230	235	240
Leu Gly Tyr Val	Leu Ala Thr Leu Leu	Leu Phe Ile Leu Leu Leu	
	245	250	255
Val Thr Val Leu	Leu Ala Ala Arg Arg	Arg Arg Gly Gly Tyr Glu	
	260	265	270
Tyr Ser Asp Gln	Lys Ser Gly Lys Ser	Lys Gly Lys Asp Val Asn	
	275	280	285
Leu Ala Glu Phe	Ala Val Ala Ala Gly	Asp Gln Met Leu Tyr Arg	
	290	295	300
Ser Glu Asp Ile	Gln Leu Asp Tyr Lys	Asn Asn Ile Leu Lys Glu	
	305	310	315
Arg Ala Glu Leu	Ala His Ser Pro Leu	Pro Ala Lys Tyr Ile Asp	
	320	325	330
Leu Asp Lys Gly	Phe Arg Lys Glu Asn	Cys Lys	
	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

cgccggagggc agcggcgggcg tggcgcgagcg gcgacatggc cgttgtctca 50
gaggacgact ttacgacag ttcaaactcc acctacggaa ccacaagcag 100
cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200
atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250
cactgccaag gactactgga tgttcaaact ccgcaactcc tccagcccag 300
ccaccgggga ggacctgag ggctcagaca tctgaacta ctttgagagc 350
taccttgccg ttgcctccac cgtgcctcc atgctgtgcc tgggtggcaa 400
cttctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450
tgacggtcat cctggccatc ttcattggtga taactgcact ggtgaagggtg 500
gacacttcct cctggaccgc tgggtttttt gcggtcacca ttgtctgcat 550
ggtgatcctc agcgggtgct ccactgtctt cagcagcagc atctacggca 600
tgaccggctc ctttctatg aggaactccc aagcactgat atcaggagga 650
gccatgggcg ggacggtcag cgccgtggcc tcattggtgg acttggtgc 700
atccagtgat gtgaggaaca ggccttggc cttcttctg acggccacca 750
tcttctctgt gctctgcatg ggactctacc tgctgtgtc caggctggag 800
tatgccaggc actacatgag gcctgttctt gcggcccatg tgtttctgg 850
tgaagaggag cttccccagg actccctcag tgccccttcg gtggcctcca 900
gattcattga ttccacaca cccctctcc gcccaccc gaagaagacg 950
gccagcctgg gcttctgtgt cacctacgtc ttcttcatca ccagcctcat 1000
ctaccccgcc gtctgcacca acatcgagtc cctcaacaag ggctcgggct 1050
cactgtggac caccaagttt ttcatcccc tcaactacct cctcctgtac 1100
aactttgctg acctatgtgg ccggcagctc accgcctgga tccaggtgcc 1150
agggcccaac agcaaggcgc tcccagggtt cgtgctctc cggacctgcc 1200
tcattcccc cttcgtgtc tgtaactacc agccccggt ccacctgaag 1250
actgtggtct tccagtccga tgtgtacccc gcactcctca gctccctgct 1300
ggggctcagc aacggctacc tcagcaccct ggccctctc tacgggccta 1350
agattgtgcc caggagctg gctgaggcca cgggagtgg gatgtccttt 1400
tatgtgtgct tgggcttaac actgggctca gcctgtctc ccctcctggt 1450

gcacctcatc tagaaggag gagacaagga cattggtgct tcagagcctt 1500
tgaagatgag aagagagtgc aggagggctg ggggccatgg aggaaaggcc 1550
taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1600
cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata 1650
ttccagtcat attaacagaa cactcctgag acagttgaag aagaaatagc 1700
acaaatcagg ggtactccct tcacagctga tggttaacat tccaccttct 1750
ttctagccct tcaaagatgc tgccagtgtt cgccctagag ttattacaaa 1800
gccagtgcc aaaccagcc atgggctott tgcaacctcc cagctgcgct 1850
cattccagct gagagcgaga tgcaagcaa tgctcagctc tccttaccct 1900
gaaggggtct ccctggaatg gaagtccctt ggcatgggtca gtcctcaggc 1950
ccaagactca agtgtgcaca gaccctgtg ttctgcggtt gaacaactgc 2000
ccactaacca gactggaaaa ccagaaaga tgggccttcc atgaatgctt 2050
cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100
ggcctgggtt ttcaaaaaaa gagggatcct catgacctgg tggctatagg 2150
cctgggtcaa gatgagggtc tttcagtgtt cctgtttaca acatgtcaaa 2200
gccattggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
1 5 10 15
Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
20 25 30
Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

	395		400		405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser					
	410		415		420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu					
	425		430		435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly					
	440		445		450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser					
	455		460		465
Ala Cys Ser Thr Leu Leu Val His Leu Ile					
	470		475		

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.
 <400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50
ctggagacac catctccac cgagagtcac ggccccattg gcctgcacc 100
tcctcgctct cgtcccatc ctctcagcc tggcggcctc ccaggactgg 150
aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggcgacctg ggggctcaat cggaccctga 250
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtggcc 300
gccaagggtg tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
taacaggatc gggggccgca tcttcaccta ccgggaccag aacacgggct 400
ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550
tggcggagaa ggtgcccag aagctgggct acgccttgcg tcccaggaa 600
aaggggcact cggccgaaga catctaccag atggctctca accaggccct 650
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700
ggcacacgct cttggaatat cttctcgagg aggggaacct gagccggccg 750
gcgctgcagc ttctgggaga cgtgatgtcc gaggatggct tcttctatct 800
cagcttcgcc gagccctcc gggccacag ctgcctcagc gacagactcc 850
agtacagccg catcgctgggt ggctgggacc tgctgccgcg cgcgctgctg 900
agctcgctgt ccgggcttgt gctgttgaac gcgcccgtgg tggcgatgac 950
ccagggaccg cacgatgtgc acgtgcagat cgagacctct cccccggcgc 1000
ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgga 1050
ccggcggtga agcgcatcac cttctcgccg ccgctgcccc gccacatgca 1100
ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttcctaa 1150
gcttcgcag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200
aacaccgatc gcccgctgcg catgattttc taccgcccgc cgcgagagg 1250
cgcgctgctg ctggcctcgt acacgtggtc ggacgcggcg gcagcgcttcg 1300
ccggcttgag ccgggaagag gcgttgcgct tggcgctoga cgacgtggcg 1350

gcattgcacg ggcctgtcgt gcgccagctc tgggacggca ccggcgtcgt 1400
 caagcgttgg gcggaggacc agcacagcca ggggtggcttt gtggtacagc 1450
 cgccggcgct ctggcaaacc gaaaaggatg actggacggt cccttatggc 1500
 cgcattctact ttgccggcga gcacaccgcc taccgcacg gctgggtgga 1550
 gacggcggtc aagtcggcgc tgcgcgccgc catcaagatc aacagccgga 1600
 aggggcctgc atcggacacg gccagccccg aggggcacgc atctgacatg 1650
 gaggggcagg ggcattgtga tggggtggcc agcagcccct cgcattgacct 1700
 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
 aaaaacacgac ccacacgagg acctcgcatt aaagtatttt cggaaaaaaa 1800
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu	1	5	10	15
Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln	20	25	30	
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu	35	40	45	
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln	50	55	60	
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala	65	70	75	
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala	80	85	90	
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn	95	100	105	
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser	110	115	120	
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu	125	130	135	
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His	140	145	150	
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys	155	160	165	

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
	545		550		555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His					
	560		565		

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
 ctgacatggc ctgactcggg acagctcaga gcagggcaga actggggaca 50
 ctctggggccg gcctttctgcc tgcattggacg ctctgaagcc accctgtctc 100
 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc ccatttcact agaagcactg agagatgcgg 200
 cccctctgca gggctctgaat ttcctgctgc tgttcacaaa gatgcttttt 250
 atctttaact ttttgttttc ccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcc ttttcttggtg gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
 ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450
 cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgtg 500
 tgtctgacaa tgggcccctgc ttgggatata gaaaaccaa ccagccctac 550
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
 ctgtctcttg cataaagggt ataatcatc accagaccag tttgtcggca 650
 tctttgctca gaataggcca gaggatgca tctccgaatt ggcttggtac 700
 acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750

catcgtacat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800
caccceaaaaa ggcattggtg ctgataggga atgtagagaa aggcttcacc 850
ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000
gacctgagcg tcatctgctt caccagtggg accacaggtg accccaaagg 1050
agccatgata acccatcaaa atattgtttc aaatgctgct gcctttctca 1100
aatgtgtgga gcatgcttat gagccactc ctgatgatgt ggccatatcc 1150
tacctccctc tggctcatat gtttgagagg attgtacagg ctggttggtgta 1200
cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250
ctgacgacat gaagactttg aagcccacat tgtttcccg cgtgcctcga 1300
ctccttaaca ggatctacga taaggtaaa aatgaggcca agacaccctt 1350
gaagaagttc ttgttgaagc tggctgtttc cagtaaattc aaagagcttc 1400
aaaagggtat catcaggcat gatagtttct gggacaagct catctttgca 1450
aagatccagg acagcctggg cggaagggtt cgtgtaattg tcaactggagc 1500
tgcccccatg tccacttcag tcatgacatt cttccgggca gcaatgggat 1550
gtcaggtgta tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600
tttacattac ctggggactg gacatcaggt cacgttgggg tgcccctggc 1650
ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700
tgaataatga aggagaggtc tgcacaaagg gtacaaaacgt gttcaaagga 1750
tacctgaagg accctgagaa gacacaggaa gccctggaca gtgatggctg 1800
gcttcacaca ggagacattg gtcgctggct cccgaatgga actctgaaga 1850
tcatcgaccg taaaaagaac attttcaagc tggcccaagg agaatacatt 1900
gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
aatttttgta cacggggaga gcttacggtc atccttagta ggagtgggtg 2000
ttcctgacac agatgtactt ccctcatttg cagccaagct tgggggtgaag 2050
ggctcctttg aggaactgtg ccaaaaccaa gttgtaaggg aagccatttt 2100
agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150
aggtcaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200

ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250
tcggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300
tacttaagta cctgccggcc cactgtgcac tgcttgtgag aaaatggatt 2350
aaaaactatt cttacatttg ttttgccctt cctcctattt ttttttaacc 2400
tgttaaactc taaagccata gcttttgctt tatattgaga catataatgt 2450
gtaaacttag ttcccaaata aatcaatcct gtctttccca tcttcogatgt 2500
tgctaataatt aaggcttcag ggctactttt atcaacatgc ctgtottcaa 2550
gatcccagtt tatgttctgt gtccttcctc atgatttcca accttaatac 2600
tattagtaac cacaagttca aggggtcaaag ggaccctctg tgccttcttc 2650
tttgttttgt gataaacata acttgccaac agtctctatg cttatttaca 2700
tcttctactg ttcaaactaa gagattttta aattctgaaa aactgottac 2750
aattcatgtt ttctagccac tccacaaacc actaaaattt tagtttttagc 2800
ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctctt 2850
ctgogtaaatt taaattgtgt actgaaggga aaagtttgat cataccaaac 2900
atttctctaaa ctctctagtt agatatctga cttgggagta ttaaaaattg 2950
ggctctatgac atactgtcca aaaggaatgc tgttcttaaa gcattattta 3000
cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050
gaagctgtgg gggaaggagt tgacaggtgg gccagtgaa cttttccagt 3100
aaatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150
acaggcaagc aagatgcccc cacaacaggc ttattttctg tgaaggaacc 3200
aactgatctc cccaccctt ggattagagt tcctgctcta ccttaccac 3250
agataacaca tggtgtttct acttgtaaatt gtaaagtctt taaaataaac 3300
tattacagat aaaaaa 3316

<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
1				5					10					15

Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
				20					25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	
				35					40					45	
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	
				50					55					60	
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	
				65					70					75	
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	
				80					85					90	
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	
				95					100					105	
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	
				110					115					120	
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	
				125					130					135	
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	
				140					145					150	
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	
				155					160					165	
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	
				170					175					180	
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	
				185					190					195	
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	
				200					205					210	
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	
				215					220					225	
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	
				230					235					240	
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	
				245					250					255	
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	
				260					265					270	
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	
				275					280					285	
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	
				290					295					300	
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	
				305					310					315	
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr	

	320		325		330
His Gln Asn Ile	Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys	Val		
	335		340		345
Glu His Ala Tyr	Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser	Tyr		
	350		355		360
Leu Pro Leu Ala	His Met Phe Glu Arg	Ile Val Gln Ala Val	Val		
	365		370		375
Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile	Arg		
	380		385		390
Leu Leu Ala Asp	Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe	Pro		
	395		400		405
Ala Val Pro Arg	Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln	Asn		
	410		415		420
Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala	Val		
	425		430		435
Ser Ser Lys Phe	Lys Glu Leu Gln Lys	Gly Ile Ile Arg His	Asp		
	440		445		450
Ser Phe Trp Asp	Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser	Leu		
	455		460		465
Gly Gly Arg Val	Arg Val Ile Val Thr	Gly Ala Ala Pro Met	Ser		
	470		475		480
Thr Ser Val Met	Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln	Val		
	485		490		495
Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr	Phe		
	500		505		510
Thr Leu Pro Gly	Asp Trp Thr Ser Gly	His Val Gly Val Pro	Leu		
	515		520		525
Ala Cys Asn Tyr	Val Lys Leu Glu Asp	Val Ala Asp Met Asn	Tyr		
	530		535		540
Phe Thr Val Asn	Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr	Asn		
	545		550		555
Val Phe Lys Gly	Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu	Ala		
	560		565		570
Leu Asp Ser Asp	Gly Trp Leu His Thr	Gly Asp Ile Gly Arg	Trp		
	575		580		585
Leu Pro Asn Gly	Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn	Ile		
	590		595		600
Phe Lys Leu Ala	Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile	Glu		
	605		610		615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
620 625 630

Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp
635 640 645

Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly
650 655 660

Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile
665 670 675

Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr
680 685 690

Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser
695 700 705

Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
710 715 720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu
725 730 735

His Ile Gln Asp

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

ggaggcggag gccgcggcga gccggggcca gcagtgaggg ccctagcggg 50
gcccagagcgg ggcccggggc ccctaagcca ttcctgaagt catgggctgg 100
ccaggacatt ggtgaccgc caatccggta tggacgactg gaagcccagc 150
cccctcatca agcccttttg ggctcggaag aagcggagct ggtaccttac 200
ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
caggggccgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300
atcctggaca ctggcgagc catcagtga gccaatgaag acccagagcc 350
agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
gaggcagtgg tccccggcgg gtccctggacg tagaggtgta ttcaagtcgc 450
agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500
ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
gccacgtgat ggcaaacgt gtgtttgaca cgtactcacc tcatgaggat 600
gaggccatgg tgctattcct caacatggta gcgccggcc gagtgctcat 650

ctgcactgtc aaggatgagg gctccttcca cctcaaggac acagccaagg 700
 ctctgctgag gagcctgggc agccaggctg gccctgccct gggctggagg 750
 gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800
 acattctaag tcacctgccc tctcttcctg gggggaccca gtcctgctga 850
 agacagatgt gccattgagc tcagcagaag aggcagagtg cacttgggca 900
 gacacagagc tgaacogtcg ccgccggcgc ttctgcagca aagttgaggg 950
 ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000
 ctgacccact ccagacaac aaggctcctca atgtgcctgt ggctgtcatt 1050
 gcagggaacc gaccaatta cctgtacagg atgctgcgct ctctgctttc 1100
 agcccagggg gtgtctcctc agatgataac agttttcatt gacggctact 1150
 atgaggaacc catggatgtg gtggcactgt ttggtctgag gggcatccag 1200
 catactccca tcagcatcaa gaatgccgcg gtgtctcagc actacaaggc 1250
 cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300
 ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350
 caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400
 ctggaatgac caggggtatg aacacacggc tgaggacca gactactgt 1450
 accgtgtgga gaccatgcct gggctgggct gggctgctcag gaggtccttg 1500
 tacaaggagg agcttgagcc caagtggcct acaccgaaa agctctggga 1550
 ttgggacatg tggatgcgga tgcctgaaca acgcccgggc cgagagtgca 1600
 tcattccctga cgtttccga tcctaccact ttggcatcgt cggcctcaac 1650
 atgaatggct actttcacga ggctacttc aagaagcaca agttcaacac 1700
 ggttccagggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750
 atgaagtgga agttcacagg ctgctcagtg aggctgaggt tctggaccac 1800
 agcaagaacc cttgtgaaga ctctttcctg ccagacacag agggccacac 1850
 ctacgtggcc tttattcgaa tggagaaaga tgatgacttc accacctgga 1900
 cccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950
 catcggggcc tgtggagatt gtttcggaag aagaaccact tcctggtggt 2000
 gggggtcccg gcttccccct actcagtga gaagccaccc tcagtcaccc 2050
 caattttcct ggagccaccc ccaaaggagg agggagcccc aggagcccca 2100


```

gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150
ccccaggct ggctagccct tccctccatc ctgtaggatt ttgtagatgc 2200
tggtaggggc tggggctacc ttgtttttaa catgagactt aattactaac 2250
tccaagggga gggttccctt gctccaacac cccgttcttg agttaaaagt 2300
ctatttattt acttccttgt tggagaaggg caggagagta cctgggaatc 2350
attacgatcc ctagcagctc atcctgccct ttgaataccc tcactttcca 2400
ggcctggctc agaatctaac ctatttattg actgtcctga ggccttgaa 2450
aacaggccga acctggaggg cctggatttc tttttgggct ggaatgctgc 2500
cctgagggtg gggctggctc ttactcagga aactgctgtg cccaacccat 2550
ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600
cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650
caaagctgga taagttggtc attgattaaa aaaggagaag ccctctggga 2700
aaaaaaaaaa aaaaaaaaaa aaaaa 2725

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400

```

<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

```

```

<400> 88

```

```

Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
1          5          10          15
Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
20        25        30
Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
35        40        45
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
50        55        60
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65        70        75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
80        85        90
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
95        100       105
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
110       115       120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125       130       135

```

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu			

	425		430		435
Asp Pro Ala Leu	Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu	Gly		
	440	445	450		
Trp Val Leu Arg	Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro	Lys		
	455	460	465		
Trp Pro Thr Pro	Glu Lys Leu Trp Asp	Trp Asp Met Trp Met	Arg		
	470	475	480		
Met Pro Glu Gln	Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp	Val		
	485	490	495		
Ser Arg Ser Tyr	His Phe Gly Ile Val	Gly Leu Asn Met Asn	Gly		
	500	505	510		
Tyr Phe His Glu	Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr	Val		
	515	520	525		
Pro Gly Val Gln	Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu	Ala		
	530	535	540		
Tyr Glu Val Glu	Val His Arg Leu Leu	Ser Glu Ala Glu Val	Leu		
	545	550	555		
Asp His Ser Lys	Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp	Thr		
	560	565	570		
Glu Gly His Thr	Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp	Asp		
	575	580	585		
Asp Phe Thr Thr	Trp Thr Gln Leu Ala	Lys Cys Leu His Ile	Trp		
	590	595	600		
Asp Leu Asp Val	Arg Gly Asn His Arg	Gly Leu Trp Arg Leu	Phe		
	605	610	615		
Arg Lys Lys Asn	His Phe Leu Val Val	Gly Val Pro Ala Ser	Pro		
	620	625	630		
Tyr Ser Val Lys	Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu	Glu		
	635	640	645		
Pro Pro Pro Lys	Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln	Thr		
	650	655	660		

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25
 <210> 90
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 90
 cctcaaccag gccacgggcc ac 22

 <210> 91
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 91
 cccaggcaga gatgcagtac aggc 24

 <210> 92
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 92
 cctccagtag gtggatggat tggctc 26

 <210> 93
 <211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 93
 ctcacatcat gaggatgagg ccatggtgct attcctcaac atggtag 47

 <210> 94
 <211> 3037
 <212> DNA
 <213> Homo sapiens

<400> 94

cggacgcgtg ggctgctggt gggaaggcct aaagaactgg aaagcccact 50
ctcttggaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100
actggaaatt tgttgtctag tgggtgtggg tgaataaagg agggcagaat 150
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200
gttacgtggc cggaatcatt cccttggtg ttaatttctc agaggaacga 250
ctgaagctgg tgactgtttt ggggtgctggc cttctctgtg gaactgctct 300
ggcagtcac gtgcctgaag gactacatgc cctttatgaa gatattcttg 350
agggaaaaca ccaccaagca agtgaaacac ataatgtgat tgcacagac 400
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500
tcatgttgct ggtggaccag attggttaact cccatgtgca ttctactgac 550
gatccagaag cagcaaggtc tagcaattcc aaaatcacca ccacgctggg 600
tctggttgtc catgctgcag ctgatggtgt tgctttggga gcagcagcat 650
ctacttcaca gaccagtgtc cagttaattg tgtttgtggc aatcatgcta 700
cataaggcac cagctgcttt tggactgggt tccttcttga tgcagctgg 750
cttagagcgg aatcgaatca gaaagcactt gctggctctt gcattggcag 800
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850
gaagcccttt cagaggtgaa cgccacggga gtggccatgc ttttctctgc 900
cgggacattt ctttatgttg ccacagtaca tgtcctccct gaggtgggag 950
gaatagggca cagccacaag ccgatgccca cgggaggag aggcctcagc 1000
cgcttggaa tggcagccct ggttctgggt tgcctcatcc ctctcatcct 1050
gtcagtagga caccagcatt aaatgttcaa ggtccagcct tggccaggg 1100
ccgtttgcc tccagtga acagccggca cgtgacagct actcacttcc 1150
tcagtctctt gtctcacctt gcgcatctct acatgtattc ctagagtcca 1200
gaggggaggt gaggttaaaa cctgagtaat ggaaaagctt ttagagtaga 1250
aacacattta cgttgcagtt agctatagac atcccattgt gttatctttt 1300
aaaaggccct tgacattttg cgttttaata tttctcttaa ccctattctc 1350
agggagatg gaatttagtt ttaaggaaaa gaggagaact tcatactcac 1400
aatgaaatag tgattatgaa aatacagtgt tctgtaatta agctatgtct 1450

ctttcttctt agtttagagg ctctgctact ttatccattg atttttaaca 1500
 tggttcccac catgtaagac tggtgcttta gcatctatgc cacatgcgtt 1550
 gatggaaggt catagcacc cactcacttag atgctaaagg tgattctagt 1600
 taatctggga ttaggggtcag gaaaatgata gcaagacaca ttgaaagctc 1650
 tctttatact caaaagagat atccattgaa aagggatgtc tagagggatt 1700
 taaacagctc ctttggcacg tgcctctctg aatccagcct gccattccat 1750
 caaatggagc aggagagggt ggaggagcct ctaaagagggt gactgggtatt 1800
 ttgtagcatt ccttgtcaag ttctcctttg cagaatacct gtctccacat 1850
 tcctagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900
 agaacagtca gatcacaaag tgtcttttga aattaaggga tattaaattt 1950
 taagtgattt ttggatgggt attgatattt ttgtagtagc tttttttaa 2000
 agactaccaa aatgtatggt tgcctttttt ttttgttttt ttttttttta 2050
 attattttct ttagcagatc agcaatccct ctagggacct aaatactagg 2100
 tcagcttttg cgacactgtg tcttctcaca taaccacctg tagcaagatg 2150
 gatcataaat gagaagtgtt tgcctattga tttaaagctt attggaatca 2200
 tgtctcttgt ctcttcgtct tttctttgct tttcttctaa cttttccctc 2250
 tagcctctcc tcgccacaat ttgctgctta ctgctgggtg taatatttgt 2300
 gtgggatgaa ttcttatcag gacaaccact tctcgaactg taataatgaa 2350
 gataataata tctttattct ttatccctt caaagaaatt acctttgtgt 2400
 caaatgccgc tttgttgagc ccttaaaata ccacctctc atgtgtaaat 2450
 tgacacaatc actaatctgg taatttaaac aattgagata gcaaaagtgt 2500
 ttaacagact aggataattt ttttttcata tttgccaaa tttttgtaaa 2550
 ccctgtcttg tcaaataagt gtataatatt gtattattaa tttattttta 2600
 ctttctatac catttcaaaa cacattacac taagggggaa ccaagactag 2650
 tttcttcagg gcagtggacg tagtagtttg taaaaacgtt ttctatgacg 2700
 cataagctag catgcctatg atttatttcc ttcattgaatt tgtcactgga 2750
 tcagcagctg tggaaataaa gcttgtaggc cctctgctgg ccacagtgag 2800
 gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850
 catacaattt tactaccaag agaaggata gtatggaaag tccaaatgac 2900

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950
 ctagtccttc aaaactatat ggttgcctag attctctctg gaaactgact 3000
 ttgtcaaata aatagcagat ttagtgtca aaaaaaa 3037

<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
 Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu
 1 5 10 15
 Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
 20 25 30
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230		235		240									
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
				245					250					255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
				275					280					285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
				290					295					300
Leu	Ser	Val	Gly	His	Gln	His								
				305										

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.
 <400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

gctcgaggcc ggcggcggcg ggagagcgac ccgggcggcc tcgtagcggg 50
gccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100
ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtgc 150
ccgccccctc tgctggccgc cctggtggcc tgcattcatc tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
tggagctgga aggcagggtc cgcaggcggc ctgcagagag aggcgccgtg 300
gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
gagaggctca tccgagtgcg gcaagaccag ttaaagacct tgcagaggaa 500
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550
acctggagag gaagttctcc tacgacctga gccagtgcatt caatcagatg 600
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcacaaaaaa 650
ggggaatgaa gctgtagctt ccagagacct gagtgaaaac aacgaccaga 700
gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750
ggcctgccac acacagaggt gccacaaggg aagggaacg tgcttggtaa 800
cagcaagtcc cagacaccag ccccagttc cgaagtgggt ttggattcaa 850
agagacaagt tgagaaagag gaaaccaatg agatccaggt ggtgaatgag 900
gagcctcaga gggacaggct gccgcaggag ccaggccggg agcaggtggt 950
ggaagacaga cctgtaggtg gaagaggctt cgggggagcc ggagaactgg 1000
gccagacccc acaggtgcag gctgccctgt cagtgagcca ggaaaatcca 1050
gagatggagg gccctgagcg agaccagctt gtcattcccc acggacagga 1100
ggaggagcag gaagctgccg gggaaggag aaaccagcag aaactgagag 1150
gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200
aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300
ggaatcatac actctgaatt gaactggaat cacatatctt acaacagggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400

gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met	Met	Gly	Leu	Gly	Asn	Gly	Arg	Arg	Ser	Met	Lys	Ser	Pro	Pro
1				5					10					15

Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
 ggatgcagaa agcctcagtg ttgctcttcc tggcctgggt ctgcttcctc 50
 ttctacgctg gcattgccct cttcaccagt ggcttcctgc tcacccgttt 100
 ggagctcacc aaccatagca gctgccaaaga gccccaggc cctgggtccc 150
 tgccatgggg gagccaagg aaacctgggg cctgctggat ggcttcccga 200
 ttttgcggg ttgtgttggt gctgatagat gctctgcgat ttgacttgc 250
 ccagccccag cattcacacg tgcctagaga gcctcctgtc tccctaccct 300
 tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
 catgccggc tctaccgatc tcagggtgac cctcctacca ccaccatgca 400
 gcgcctcaag gccctacca ctggctcact gcctaccttt attgatgctg 450
 gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500

ctcaccagtg caggaaggcg tgtagtcttc atgggagatg atacctggaa 550
 agaccttttc cctggtgctt tctccaaagc tttcttcttc ccatccttca 600
 atgtcagaga cctagacaca gtggacaatg gcatcctgga acacctctac 650
 cccaccatgg acagtgggtga atgggacgtg ctgattgctc acttcctggg 700
 tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750
 agaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800
 gagaatgaca cactgctggt agtggctggg gaccatggga tgaccacaaa 850
 tggagaccat ggaggggaca gtgagctgga ggtctcagct gctctctttc 900
 tgtatagccc cacagcagtc ttccccagca ccccaccaga ggagccagag 950
 gtgattcctc aagttagcct tgtgcccacg ctggccctgc tgctgggcct 1000
 gcccatccca tttgggaata tcggggaagt gatggctgag ctattctcag 1050
 ggggtgagga ctcccagccc cactcctctg ctttagccca agcctcagct 1100
 ctccatctca atgctcagca ggtgtcccga tttcttcata cctactcagc 1150
 tgctactcag gaccttcaag ctaaggagct tcatcagctg cagaacctct 1200
 tctccaaggc ctctgctgac taccagtggc ttctccagag cccaagggg 1250
 gctgaggcga cactgcccac tgtgattgct gagctgcagc agttcctgcg 1300
 gggagctcgg gccatgtgca tcgagtcttg ggctcgtttc tctctggtcc 1350
 gcatggcggg gggactgct ctcttggtg cttcctgctt tatctgcctg 1400
 ctggcatctc agtgggcaat atccccaggc tttccattct gccctctact 1450
 cctgacacct gtggcctggg gcctggttgg ggccatagcg tatgctggac 1500
 tcctgggaac tattgagctg aagctagatc tagtgcttct aggggctgtg 1550
 gctgcagtga gctcattcct cctttttctg tggaaagcct gggctggctg 1600
 ggggtccaag aggccctgg caaccctgtt tcccatccct gggcccgtcc 1650
 tgttactcct gctgtttcgc ttggctgtgt tcttctctga tagttttgtt 1700
 gtagctgagg ccagggccac ccccttcctt ttgggctcat tcatcctgct 1750
 cctggttgct cagcttctact gggagggcca gctgcttcca cctaagctac 1800
 tcacaatgcc ccgccttggc acttcagcca caacaaaccc cccacggcac 1850
 aatggtgcat atgcctgag gcttgaatt gggttgcttt tatgtacaag 1900
 gctagctggg ctttttcctc gttgcctga agagacacct gtttgccact 1950

cctctccctg gctgagtcct ctggcatcca tggtaggtgg tcgagccaag 2000
aatttatggt atggagcttg tgtggcgggc ctggtggccc tgtagctgc 2050
cgtgcgcttg tggcttcgcc gctatggtaa tctcaagagc cccgagccac 2100
ccatgctctt tgtgcgctgg ggactgcccc taatggcatt gggtagctgc 2150
gcctactggg cattggcgctc gggggcagat gaggtcctcc cccgtctccg 2200
ggctcctggc tctggggcat ccatgggtgc gcctcgggct gtagcagggc 2250
tggctgcttc agggctcgcg ctgctgctct ggaagcctgt gacagtgcgtg 2300
gtgaaggctg gggcaggcgc tccaaggacc aggactgtcc tcactccctt 2350
ctcaggcccc cccacttctc aagctgactt ggattatgtg gtccctcaaa 2400
tctaccgaca catgcaggag gagttccggg gccggttaga gaggaccaa 2450
tctcagggtc ccctgactgt ggctgcttat cagttgggga gtgtctactc 2500
agctgctatg gtcacagccc tcacctgtt ggcttccca cttctgctgt 2550
tgcagcgga gcgcacagc cttgtgttcc tgcttctgtt tctgcagagc 2600
ttccttctcc tacatctgct tgctgctggg ataccogtca ccaccttg 2650
tccttttact gtgcatggc aggcagtctc ggcttgggccc ctcatggcca 2700
cacagacctt ctactccaca ggccaccagc ctgtctttcc agccatccat 2750
tggcatgcag ccttcgtggg attcccagag ggtcatggct cctgtacttg 2800
gctgcctgct ttgctagtgg gagccaacac ctttgcctcc cacctcctct 2850
ttgcagtagg ttgcccactg ctctgctct ggcttttct gtgtgagagt 2900
caagggctgc ggaagagaca gcagcccca gggaatgaag ctgatgccag 2950
agtcagaccc gaggaggaag aggagccact gatggagatg cggctccggg 3000
atgcgcctca gcacttctat gcagcactgc tgcagctggg cctcaagtac 3050
ctctttatcc ttggtattca gattctggcc tgtgccttgg cagcctccat 3100
ccttcgcagg catctcatgg tctggaaagt gtttgcctc aagttcatat 3150
ttgaggctgt gggcttcatt gtgagcagcg tgggacttct cctgggcata 3200
gctttggtga tgagagtgga tgggtgctgt agctcctggg tcaggcagct 3250
atctctggcc cagcagaggt agcctagtct gtgattactg gcacttggtc 3300
acagagagtg ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350
atctgcaaga caggctcagc catactctta ctatcatgca gccaggggcc 3400

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450
 tgatccctaa ctcttgattt ggatgcatct gagggacaag gggggcggtc 3500
 tccgaagtgg aataaaatag gccgggcgtg gtgacttgca cctataatcc 3550
 cagcactttg ggaggcagag gtgggaggat tgcttgggcc caggagttca 3600
 agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650
 agtgtaataa aatgataata t 3671

<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe
 1 5 10 15
 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
 20 25 30
 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
500		505	510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515		520	525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530		535	540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545		550	555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560		565	570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575		580	585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590		595	600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605		610	615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620		625	630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635		640	645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650		655	660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665		670	675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680		685	690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695		700	705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710		715	720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725		730	735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740		745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755		760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770		775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

	785		790		795
Val Val Pro Gln	Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly			
	800		805		810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala			
	815		820		825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu			
	830		835		840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile			
	845		850		855
Ser Leu Val Phe	Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu			
	860		865		870
His Leu Leu Ala	Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe			
	875		880		885
Thr Val Pro Trp	Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr			
	890		895		900
Gln Thr Phe Tyr	Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile			
	905		910		915
His Trp His Ala	Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser			
	920		925		930
Cys Thr Trp Leu	Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala			
	935		940		945
Ser His Leu Leu	Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp			
	950		955		960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro			
	965		970		975
Pro Gly Asn Glu	Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu			
	980		985		990
Glu Pro Leu Met	Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe			
	995		1000		1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu			
	1010		1015		1020
Gly Ile Gln Ile	Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg			
	1025		1030		1035
Arg His Leu Met	Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe			
	1040		1045		1050
Glu Ala Val Gly	Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly			
	1055		1060		1065
Ile Ala Leu Val	Met Arg Val Asp Gly	Ala Val Ser Ser Trp Phe			
	1070		1075		1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgcct aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactocaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaacgtggc ccagtggtg gaccaaccac acgctggtgc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gagggcccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtccct 950
cagcagaaca ataccocccg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtgcg aggcagcggt 1100
ggcagtcttg ggcccgcgaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccc 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
 agccttctga ggggatggg ctggagagg agggcttct atctagactc 1350
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400
 catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450
 gccaacactt ccttttgct tttgtttcct gtgcaaacia gtgagtcacc 1500
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550
 ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
 cgtgtgtgat tggttcatgc atgtaggctt cttacaatg atgggtgggc 1650
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
1				5					10					15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	425	430	435
Leu	Tyr	Val	Gln	Met	Glu	Asn									440		

<210> 105

```

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

```

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaakat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggccggacgcg tgggcccgcg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccaccg ccctgatgct gcccgtgaag cccccgcag 150
gctcctgggg ggcccagatc atcggggggc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttctgtctg cgagcccgt ggggtggtctc ggccgcccac tgcttcagcc 300
acagagacct ccgactggc ctggtggtgc tgggcgcca cgtcctgagt 350
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccagca 400
ccccgactac caccatga cccacgcca cgacatctgc ctgctgcggc 450
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcc 500
gggagaaggg ccaggcccc cacagcggg acacggtgcc gggtggtgg 550
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600
ccaaggtccg agtgtggac ccggacgtct gcaacagctc ctggaagggc 650
cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700
gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750
ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800
cccgacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850
ggttcggcgg agcagtcccc agcccgccc cctgcctggg accaccaggc 900
ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
gccgctccag gcctggaatg ttccgtggct gggcccccacg ggaagcctga 1000
tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
1 5 10 15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
cctgacgcct gacgcctgtc cccggcccgc catgagccgc tacctgctgc 100
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggtctt cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
 tgctggacaa gctgaaagcc tcagcccctt cgcgatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
 gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
 cacgggcatc catggtctca ctttctccag caccacactc gggcccatct 850
 tctggctgct ggtcaagagc cccgagctgg ccgcccagcc cagcacatac 900
 ctggccgtgg cggaggaact ggcggatggt tccggaaagt acttcgatgg 950
 actcaaacag aaggccccgg cccccgaggc tgaggatgag gaggtggccc 1000
 ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050
 gtgagggagc agcccctccc cagataacct ctggagcaga tttgaaagcc 1100
 aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgagcttc 1150
 ctggcactac ctgagccggg agaccagga ctggcgccg ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
 gcactgcccc gggtctctggc tggttccgtc tgctctgctg ccagcagggg 1300
 agagggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350
 ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcggg 1400
 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450
 tctgacactt ggtggattct tgggtccctg tgggaccttg tgcattgatg 1500
 gtctctctct agccttgggt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatgggtgt gtacagcgag ctgttgtctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgagggtt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccaggttc aggctctgca cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230						235				240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117

<211> 2249

<212> DNA

<213> Homo sapiens

<400> 117

```

gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggcgctg 50
ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgaggctcg 100
gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
agcgccggct gctggggctg ctgaggcggc acctgcgcgg ggaggaggcg 200
cggtgcggg acctgactag attctacgac aaggctactt ctttgcata 250
ggattcaaca acccctgtgg ctaaccctct gcttgcatct actctcatca 300
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
gagaacatoc gagctctgaa ggatggctat gagaagggtg agcaagacct 400
tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450
aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
agagtcactg gctctgcat cactgacctg tacagcccca aacggctctt 550
ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
tgggggatta ttaccatgcc attccatggc tggaggaggc tgcagtctc 650
ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

```

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 cccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgctctc taccatgact tcgtcagtga ctacagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac caaaactgg tgaccctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcaactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700
 aagccaggag caaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaa tcagaggcaa 1800
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtggg 1900
 ggctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctgact ccagaaactt taagactttc tccccactgc cttctgctgc 2100
 agccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu		245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr		260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala		275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr		290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr		305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala		320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu		335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala		350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val		365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser		380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr		395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro		410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly		425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro		440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile		455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr		470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp		485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His		500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys		515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser				

530

535

540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtacttttctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagataggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50

tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100

gaatcgggcc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc ggcgcgttct cctacctctg 250
 gctcaagttt tcaattatca tctattccac cgtgttcttg ctgattgggg 300
 ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
 gggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagtgc 650
 aagtgtctgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gccctggac cctggcctg tggggtgccc tacacctgct 750
 gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
 atcgacaagg agcggttctag tgtgcaggat gtcattctacg tgcggggctg 850
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
 gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
 ctgctgtaca tcacccgggt ggaggacatc atcatggagc actctgtcac 1000
 tgatgggctc ctggggcccc gtgccaagcc cagcgtggag gcggcaggca 1050
 cgggatgctg cttgtgtctac cccaattagg gccagcctg ccatggcagc 1100
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
 ggacagggct ggggccctc tgccacact cagtactgac caaagccagg 1200
 gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc ccagggagc 1250
 agagcctggg cctcccctaa gaggctttcc ccgaggcagc tctggaatct 1300
 gtgcccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350
 ctacagggga gggagagcct gaggctctgc tcagggccca tttcatctct 1400
 ggcagtgcct tggcgggtgtt attcaaggca gttttgtagc acctgtaatt 1450
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccagggttggc 1550
 ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggctgct 1600
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgcccttccc ccaaccagtt tgттаatcaa acaataaaaa 1750
 catgttttgt ttgttttta aaaaaaaa 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggcg gcccgaggac cttcacccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccacc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggtc atcacagcta 350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450
gaccatcgtg gagttocaca tgacgactga ggccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgcc tggtcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
ggcatgtatg cagacctcct gcagctggtg aaggtgccca tttccctcag 750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaattgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggtcctgtt ggactctgtg 1000
cttcctgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100
aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150
ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200
caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggg cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcttcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
 gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
 1 5 10 15
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
 20 25 30
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480
Pro Val Ser Gln																	

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcggtttt ggtgtgtctc tgtgaccatg 50
gtgggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100
aaagaaggag atggtgttat ctgaaaagg tagtcagctg atggaatgga 150
ctaacaaaag acctgtata agaataaat gagacaagtt ccgtcgcctt 200
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctc 250
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
ttttttgcc tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
tagaccccc aattatgctg gtccccttat gttgggattg cttttggctg 600
ttattgggtg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650
aataaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750
atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
agcgaaagat aatgtgtgtg gctggatttg gacttggtgt attattcttc 950
agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000
ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100
gtatatattt tattacctct ttttttcaag tgatttaaat agttaatcat 1150
ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaaat 1200
ctgaggtatt tgaaaataat tatcctctta accttctctt ccagtgaaac 1250
tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300
aactactact ttgttttagt tagaacaag ctcaaaacta ctttagttaa 1350
cttggtcac tgattttata ttgccttacc caaagatggg gaaagtaagt 1400
cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450

```

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcac 1500
tttccttttg agtagagaaa ttatgtgtgt catgtggctt tctgaaaatg 1550
gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600
ctcctcctcc ttgcatattt cctactgcg cccagcctga gtgatagagt 1650
gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
gcttgagtat ggtgttaact acctgtatt tagaaagatt tcagattcat 1750
tccatctcct tagttttctt ttaaggtgac ccatctgtga taaaaatata 1800
gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850
aaattagagt ttgtcactta ttccatttgt acctagaga aaaataggct 1900
cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100
tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150
agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
aaaaaaaaaa aaa 2213

```

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

```

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
 1          5          10          15
Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20          25          30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35          40          45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50          55          60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65          70          75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80          85          90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95          100         105

```

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
				320					325					330	
Ser	Phe	Leu	Met	Ser											
				335											

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

aagcaaccaa actgcaagct ttgggagttg ttcgctgtcc ctgccctgct 50

ctgctagggg gagaacgcca gagggaggcg gctggcccgg cggcaggctc 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
 aggttaacat ttcatccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
 atggatggat gtcatggaga ggcatggcta ccgaacacag aaatttgga 500
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600
 taatcttata cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
 agaatacaga caaagcagta aactggttaa gaaaggaagc aattaattac 700
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
 ttcaccatct tctggagaaa attttgatc ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850
 tcacctttgt cagaaatgca ccctgtagat tattactott cttatacaaa 900
 aaactgcact ggaagattta caaaaaaga aattaagaat attagagcat 950
 tttattatgc tatgtgtgct gagacagatg ccatgcttg tgaaattatt 1000
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
 gcattgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150
 attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250
 gatactcttt gttgccgta tcatcagaaa catttaagaa tgaacataaa 1300
 gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400
 cctattcgga tgggtcatca atattgcctc aactctttga tctttcctcg 1450
 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
 ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750
 ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800
 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtgggtcac 1850
 acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900
 aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
 aaatacaaaa attagctggg cgcggtgggt cacacctata gtctcagcta 2000
 ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050
 agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
 tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200
 aatcacatat tttcaaaaat ggttattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
 taaaatagtt gtatgtgagc atttgatggg gaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
 1 5 10 15
 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly
				80					85					90

Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu
				95					100					105

Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly
				110					115					120

Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His
				125					130					135

His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala
				140					145					150

Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg
				155					160					165

Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr
				170					175					180

Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr
				185					190					195

Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr
				200					205					210

Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His
				215					220					225

Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys
				230					235					240

Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr
				245					250					255

Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys
				260					265					270

Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu
				275					280					285

Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu
				290					295					300

Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly
				305					310					315

Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr
				320					325					330

Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile
				335					340					345

Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile
				350					355					360

Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

365	370	375
Leu Ser Gly Tyr Ser 380	Leu Leu Pro Leu Ser 385	Ser Ser Glu Thr Phe Lys 390
Asn Glu His Lys Val 395	Lys Asn Leu His Pro 400	Pro Trp Ile Leu Ser 405
Glu Phe His Gly Cys 410	Asn Val Asn Ala Ser 415	Thr Tyr Met Leu Arg 420
Thr Asn His Trp Lys 425	Tyr Ile Ala Tyr Ser 430	Asp Gly Ala Ser Ile 435
Leu Pro Gln Leu Phe 440	Asp Leu Ser Ser Asp 445	Pro Asp Glu Leu Thr 450
Asn Val Ala Val Lys 455	Phe Pro Glu Ile Thr 460	Tyr Ser Leu Asp Gln 465
Lys Leu His Ser Ile 470	Ile Asn Tyr Pro Lys 475	Val Ser Ala Ser Val 480
His Gln Tyr Asn Lys 485	Glu Gln Phe Ile Lys 490	Trp Lys Gln Ser Ile 495
Gly Gln Asn Tyr Ser 500	Asn Val Ile Ala Asn 505	Leu Arg Trp His Gln 510
Asp Trp Gln Lys Glu 515	Pro Arg Lys Tyr Glu 520	Asn Ala Ile Asp Gln 525
Trp Leu Lys Thr His 530	Met Asn Pro Arg Ala 535	Val

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
 gagagaagtc agcctggcag agagactctg aaatgagggg ttagaggtgt 50
 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagaccctt tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccagagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tctgctcat cccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
 gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 cagggatatgt gtgaagaacc agggggcaga gctgggggggt ggctgggtct 850
 gtgaaaaaca gtggacagca ccccgagggc cacaggtgag ggacactacc 900
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
 gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
 ccccaaacc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
 ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg 1350
 actccacagt gtccagacta atttgatcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Pro Ala
65	70	75
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser Ala Ile
80	85	90
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Arg Cys Thr
95	100	105
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala Val Ala
110	115	120
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe Ile Pro
125	130	135
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr Ser Pro
140	145	150
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala Leu Tyr
155	160	165
Leu Gly Ile Ile Ser	Ser Ser Leu Phe Ser	Leu Ile Ala Gly Ile Ile
170	175	180
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn Tyr Tyr
185	190	195
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser Pro Arg
200	205	210
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser Tyr Ser
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
 gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50
 cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100
 aagtcacgcg tcccgtggc tcagaaccat ggctgtgcca gccggcaccc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcca atgtggtccc cctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300
 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
 ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
 gtcttttgcca ttttctgcat ctccaggctc ctctgtctac acggagcccc 100
 agtggccccc atgaactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctcagcccgg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgttttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
1				5					10					15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20					25						30

Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45

Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60

Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75

Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90

Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105

Cys	Arg	Ser	Val	Ser
				110

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

gggggcgggg gcctggagca cggcgctggg gccgcccga ggcgtcactc 50
 gctcgcactc agtcgcggga ggcttccccg cgccggccgc gtcccggccg 100
 ctccccggca ccagaagtcc ctctgcgcgt ccgacggcga catggggctc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgcctctcgc 200
 tctcttcttg gctgcgtccc taggtccggg ggcagccttc aaggctcgcc 250
 cgccgtattc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggcccctg ggacaaagg cacgatgtga ccttctacaa 350
 gacgtggtac cgcagctcga ggggcgagg gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcacg ttccaggacc ttacacctga ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgttgga tagcggcctc tactgtgtgc tgggtggtgga gatcaggcac 600
 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
 atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750
 ggaatcctct gcctccccct catcctgtc ctggtctaca agcaaaggca 800
 ggcagcctcc aaccgccgtg ccaggagct ggtgcggatg gacagcaaca 850
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900
 atacccgagg ccaaagtcag gcacccctg tcctatgtgg ccagcggca 950
 gccttctgag tctggggcgc atctgcttcc ggagcccagc accccctgt 1000
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050
 gactctcaa actttgagg catctagccc agctggggga cagtgggctg 1100
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150
 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200
 gatactgtga catcccagaa gccagcccc tcaacccctc tggatgctac 1250
 atggggatgc tggacggctc agccctgtt ccaaggattt tggggtgctg 1300
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tggggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500
 ccccgctggcc gccttggtc ccccggtttg cccgaggctg ctcttctgtc 1550
 agacttcctc tttgtaccac agtggtctctg gggccaggcc tgcttgcctc 1600
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650
 gatctgtcaa cagggttaagt caatctgggg cttccactgc ctgcattcca 1700
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800
 gttgccccac ccactggaga tgggtctgag ggaggtgggt ggggccttct 1850
 gggaagggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccacctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	1	5	10	15
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	20	25	30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	35	40	45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	50	55	60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	65	70	75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	80	85	90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	95	100	105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	110	115	120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	125	130	135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu				

290 295 300

Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro
305 310 315

Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg
320 325 330

Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser
335 340 345

Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala
350 355 360

Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu
365 370 375

Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His
380 385 390

Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala
395 400 405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
440 445 450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
 ctagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50
 cggggagctc ccgtgggagc tccgctggct gtgcaggcgg ccatggattc 100
 cttgcggaaa atgctgatct cagtcgcaat gctgggagca ggggctggcg 150
 tgggctacgc gtcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgccg 400
 gaccttggct tgggagcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500
 gtgagctgcc gtccgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50
 ttgaggggaa gaggtgact gtacgttcct totactctgg caccactctc 100
 caggctgcc a tggggccag caccctctc ctcatottgt tctttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacctgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
 tggaggccct gggaccaaag gcaaggggaag aaggaatgag aagtacgata 500
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600
 gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650
 ttgtcttccc aaggctgctg gacttcaccc ttgccatggc tgcccggaaa 700
 gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
 aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900
 cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
 accatgtccc agagagaatg ctgaggctgc ctttgtcctc tgtgggaccc 1100
 tctatgtcgt ctataacacc cgtcctgcca gtggggcccg catccagtgc 1150
 tcttttgatg ccagcggcac cctgaccct gaacgggcag cactccctta 1200
 ttttcccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
 catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400
 ttctcattc ttcaaagtgt ggccagttgt ggctcaaac ctctatattt 1450
 ttagccaatg gcaatcaaat tctttcagct cttttgtttc atacggaact 1500
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
 ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
 cccagacca gggctctaac cttgtatgcg ggcaggcca gggagcaggc 1650
 agcagtgttc ttcccctcag agtgacttgg ggaggagaa ataggaggag 1700
 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5					10					15
Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50
 ccgctcaogc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctoctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc agtggtttgg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctoct 300
 gtttctctgtc tctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggt tccccggcc cacagcgaag tggaaaggct cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgtcatct gagccgagag gtggaatcca gggtagagat 850
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950
 ttcttctcca aattccagt gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gtcacccga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggctt tcagagtttc caagcaggga 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggt gcgcgtggga 1250
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttatc agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
 aaatgaccag tcccttattt atacctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttgga 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700
 acattcttct ttagggatat taaggctctct ctcccagatc caaagtcccg 1750
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850
 cattacattt agtttgcct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgta tcctaatggg ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

[illegible]

<210>	149
<211>	24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgcg aggettccct 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggtgccggc ggggccgcgg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttcoccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggttt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacia aggaggatga 1000
gggtcataga ttacaaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggtt 1200
ttcaggcatg aaacctgcta ggaggttttag aaatgttctt atgtttatta 1250
atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatttaac tagtggttag tagactggtt ttactctatt 1400
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaat ctagtggaaat aatgtactgt 1500
tatctaagca ttgacctgt actgcactga aagtaattat tctttgacct 1550
tatgtgaggg acttggtttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750
taaataagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atactttagc 1900
 actaaatatt ttaaattgctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctcacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctc 2100
 ctactaaaaa tacaacaaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggagggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agaggggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
 1 5 10 15

Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
 20 25 30

Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
 35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
 50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
 65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
 80 85 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
 95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
 110 115 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
 125 130 135

Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
 140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
 155 160 165

Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys	Asn		
	185		190		195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln	Thr		
	200		205		210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His	Cys		
	215		220		225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly	Leu		
	230		235		240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile	Pro		
	245		250		255

Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 154

aactgctctg tggttggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-38

<223> Synthetic construct.

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggcttt ggtotcgggtg cccagggccc aggccgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgcc a tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcc a tcatcttcac tcagctggag 400
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctgtgc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
 gggctctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

```

aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg ccctgctctt gggggaggga gagggcggaa ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cggtcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacct 200
tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaactctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcacccaca 650
gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

```

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtg tggggggagc 1100
 tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag 1150
 tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttcocaga tgggtgaagcc ttgggactcg cggggacagg aggccactga 1400
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatTTTTT taactaaaag 1650
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

110
 115
 120
 125
 130
 135
 140
 145
 150
 155
 160
 165
 170
 175
 180
 185
 190
 195
 200
 205
 210
 215
 220
 225
 230
 235
 240
 245
 250
 255
 260
 265
 270
 275
 280
 285
 290
 295
 300
 305
 310
 315
 320
 325
 330
 335
 340
 345
 350
 355
 360
 365
 370
 375
 380
 385
 390
 395
 400
 405

Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu
				125					130					135
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile
				140					145					150
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser
				155					160					165
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp
				170					175					180
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser
				185					190					195
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser
				200					205					210
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn
				215					220					225
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr
				230					235					240
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly
				245					250					255
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu
				260					265					270
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu
				275					280					285
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser
				290					295					300
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala
				305					310					315
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln
				320					325					330
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val
				335					340					345
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe
				350					355					360
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys
				365					370					375
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu
				380					385					390
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr
				395					400					405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gtcggcctg gccgctgcc tgctcttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgccca ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200

Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg	20	25	30
				35					40					45			
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly			
				50					55					60			
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile			
				65					70					75			
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr			
				80					85					90			
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro			
				95					100					105			
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly			
				110					115					120			
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr			
				125					130					135			
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys			
				140					145					150			
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser			
				155					160					165			
Cys	Val	Pro	Glu	His													
				170													

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatt acaggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctoccaaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 181
 gtgttctgct ggagccgatg cc 22

<210> 182
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatacctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
 atactttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200
 aacgccaggc atgggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctotca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65					70					

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtaggggggc acaggggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700
atgcctgcca ggggtgattct gggggccccc tgggtgtgtg gggagtcctt 750
caaggtctgg tgcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
 ccctagctcc actcttggtg gcctgggaac ttcttgaac tttaactcct 1000
 gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
 ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggt acaggagggg 400
 tcagtgaac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg acccgcctg gactccccag ccttcccacc ccatacctcc 600
 ctcccgatct tgetgccctt cttgacacac tgtgatctct ctctctctca 650
 tttgttttgt cattgagggt ttgttttgtt tttcatcaat gtctttgtaa 700
 agcaciaaatt atctgcctta aaggggtctt gggtcgggga atcctgagcc 750
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850
 cttccagcct gtgttcccct cacttgaggg aaccagcact ctccatcctt 900
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
 gacccaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000
 cctctttcgg gtttccttgg acagtgccat ggttcagtg ctctggtgtc 1050

acccaggaca cagccactog gggccccgct gccccagctg atccccactc 1100
 attccacacc ttttctcact ctcagtgatg tgaaggtggg aaggaaagga 1150
 gcttggcatt gggagocctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15

Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30

Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45

Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60

Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

cgcgctcccc ggcgcctcc tggggctcca cgcgctcttg cccgcagagg 50
cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
ggggctggcg ccgcctgctg cgcgcgctg gcgctggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttctt 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400
gacctgaagc agctagagcg actgcgctg aacaagaata agctgcaagt 450
ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagatccag gggatcccg ggaaggcgtt ccgoggcatc 550
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
acaacaacat cagtcgcatc ctggtcacca gcttcaacca catgccgaag 700
atccgaactc tgcgcctcca ctccaaccac ctctactgog actgccacct 750
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcgatgtg 850
cagaagaagg agtacgtgtg cccagcccc cactcggagc ccccatcctg 900
caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950
tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050
tgcaggagcc ttcaccagt acaagaaact gaagcgaata gacatcagca 1100
agaatcagat atcggatatt gctccagatg ccttccaggg cctgaaatca 1150
ctcacatcgc tggctcctgta tgggaacaag atcaccgaga ttgccaaggg 1200
actgtttgat gggctggtgt ccctacagct gctcctcctc aatgccaaca 1250
agatcaactg cctgcgggtg aacacgtttc aggacctgca gaacctcaac 1300
ttgctctccc tgtatgacaa caagctgcag accatcagca aggggctctt 1350
cgcccctctg cagtccatcc agacactcca cttagcccaa aaccatttg 1400
tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450

atcgagacaa gcggggcccg ctgcagcagc ccgcgccgac tcgccaacaa 1500
 gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550
 attaccgcag caggttcagc agcgagtgtc tcatggacct cgtgtgcccc 1600
 gagaagtgtc gctgtgaggg cacgattgtg gactgctcca accagaagct 1650
 ggctccgcac ccaagccacc tccctgaata tgtcaccgac ctgcgactga 1700
 atgacaatga ggtatctgtt ctggaggcca ctggcatctt caagaagttg 1750
 cccaacctgc ggaaaataaa tctgagtaac aataagatca aggaggtgcg 1800
 agagggagct ttcgatggag cagccagcgt gcaggagctg atgctgacag 1850
 ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtggc 1900
 ctcaaaacct tgatgctgag gagtaacttg atcagctgtg tgagtaatga 1950
 cacctttgcc ggctgagtt cggtagact gctgtccctc tatgacaatc 2000
 ggatcaccac catcaccctt ggggccttca ccacgcttgt ctccctgtcc 2050
 accataaacc tcctgtccaa ccccttcaac tgcaactgcc acctggcctg 2100
 gctcggcaag tggttgagga agaggcggat cgtcagtggg aaccctaggt 2150
 gccagaagcc atttttcctc aaggagattc ccatccagga tgtggccatc 2200
 caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250
 gcgctgcccc gagcagtgca cctgtatgga gacagtgggt ogatgcagca 2300
 acaaggggct ccgcgccctc cccagaggca tgcccaagga tgtgaccgag 2350
 ctgtacctgg aaggaaacca cctaacagcc gtgccagag agctgtccgc 2400
 cctccgacac ctgacgctta ttgacctgag caacaacagc atcagcatgc 2450
 tgaccaatta caccttcagt aacatgtctc acctctccac tctgacctg 2500
 agctacaacc ggctgaggtg catccccgtc cacgccttca acgggctgcg 2550
 gtccctgcga gtgctaacct tccatggcaa tgacatttcc agcgttcctg 2600
 aaggctcctt caacgacctc acatctcttt cccatctggc gctgggaacc 2650
 aaccactcc actgtgactg cagtcttcgg tggctgtcgg agtgggtgaa 2700
 ggcggggtac aaggagcctg gcatcgcccc ctgcagtagc cctgagccca 2750
 tggctgacag gtcctgtctc accaccccaa cccaccgctt ccagtgcaaa 2800
 gggccagtgg acatcaacat tgtggccaaa tgcaatgcct gcctctccag 2850
 cccgtgcaag aataacggga catgcaccca ggaccctgtg gagctgtacc 2900

catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagcg 4400
gcgagcactg ccaacaagag aatccgtgcc tgggacaagt agtccgagag 4450
gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500
gcccacatcg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550
cccgcagcaa gcggcggaag tacgtcttcc agtgcacgga cggtctctcg 4600
tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgtgtc 4650
ctaagcccct gccgcctgc ctgccacctc tcggactcca gcttgatgga 4700
gttgggacag ccatgtggga ccccttggtg attcagcatg aaggaaatga 4750
agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800
aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
1 5 10 15

Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
20 25 30

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
35 40 45

Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60

Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75

Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90

His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105

Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120

Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135

Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150

Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

	455		460		465
Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser			
	470	475			480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe				
	485	490			495
Ser Ser Glu Cys	Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg				
	500	505			510
Cys Glu Gly Thr	Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg				
	515	520			525
Ile Pro Ser His	Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn				
	530	535			540
Asp Asn Glu Val	Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys				
	545	550			555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys				
	560	565			570
Glu Val Arg Glu	Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu				
	575	580			585
Leu Met Leu Thr	Gly Asn Gln Leu Glu Thr Val His Gly Arg Val				
	590	595			600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn				
	605	610			615
Leu Ile Ser Cys	Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser				
	620	625			630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr				
	635	640			645
Pro Gly Ala Phe	Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu				
	650	655			660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly				
	665	670			675
Lys Trp Leu Arg	Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys				
	680	685			690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala				
	695	700			705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln				
	710	715			720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val				
	725	730			735
Val Arg Cys Ser	Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met				
	740	745			750

Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
				755					760					765	
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile	
				770					775					780	
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe	
				785					790					795	
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	
				800					805					810	
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu	
				815					820					825	
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu	
				830					835					840	
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly	
				845					850					855	
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu	
				860					865					870	
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser	
				875					880					885	
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr	
				890					895					900	
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala	
				905					910					915	
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr	
				920					925					930	
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr	
				935					940					945	
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile	
				950					955					960	
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser	
				965					970					975	
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly	
				980					985					990	
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	
				995					1000					1005	
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys	
				1010					1015					1020	
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile	
				1025					1030					1035	
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys	

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser	1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp	1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly	1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu	1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn	1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser	1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly	1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg	1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala	1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln	1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln	1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu	1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser	1520		

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gcccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 200

ttgttgcat tgaggaggag cagc 24

<210> 201

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 201

gagggcacg tcgaaatag cctagaacag aactccatca aagccatccc 50

<210> 202

<211> 753

<212> DNA

<213> Homo sapiens

<400> 202

ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50

gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150

cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200

atctacactc gttgcaaaact ggcaaaaata ttctcgaggg ctggcctgga 250

caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300

agagcggcta caacaccaca gcccgcagcg tcctggatga cggcagcatc 350

gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400

gctgaaggag aacaaccact gccatgtgcg ctgctcagcc ttgatcactg 450

atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500

caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550

cctgtccgag tggaaaaaag gctgtgaggt ttctctaaact ggaactggac 600

ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650

cctgtgtcat cttgtcccg ttcctcccaa tttccttct caaacttgga 700

gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750

gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcattgtgt aaaaacgcc aagctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc	ttttcttaaa	cgactataca	gggcccgaat	tgactggata	300
gaggaataca	ccacaggcat	ggcagactgc	atcttagtca	acagccagtt	350
cacagctgct	gtttttaagg	aaacattcaa	gtccctgtct	cacatagacc	400
ctgatgtcct	ctatccatct	ctaaatgtca	ccagctttga	ctcagttggt	450
cctgaaaagc	tggatgacct	agtccccaag	gggaaaaaat	tcctgctgct	500
ctccatcaac	agatacgaaa	ggaagaaaaa	tctgactttg	gcactggaag	550
ccctagtaca	gctgcgtgga	agattgacat	cccaagattg	ggagaggggt	600
catctgatcg	tggcagggtg	ttatgacgag	agagtcctgg	agaatgtgga	650
acattatcag	gaattgaaga	aaatgggtcca	acagtccgac	cttggccagt	700
atgtgacctt	cttgagggtct	ttctcagaca	aacagaaaat	ctccctcctc	750
cacagctgca	cgtgtgtgct	ttacacacca	agcaatgagc	actttggcat	800
tgcccctctg	gaagccatgt	acatgcagtg	cccagtcatt	gctgttaatt	850
cgggtggacc	cttggagttc	attgaccaca	gtgtcacagg	gtttctgtgt	900
gagcctgacc	cggtgcactt	ctcagaagca	atagaaaagt	tcatccgtga	950
accttcctta	aaagccacca	tgggcctggc	tggaagagcc	agagtgaagg	1000
aaaaattttc	ccctgaagca	tttacagaac	agctctaccg	atatgttacc	1050
aaactgctgg	tataatcaga	ttgtttttta	gatctccatt	aatgtcattt	1100
ttatggattg	tagaccaggt	tttgaaacca	aaaaagaaac	ctagaatcta	1150
atgcagaaga	gatcttttta	aaaataaact	tgagtottga	atgtgagcca	1200
ctttcctata	taccacacct	ccctgtccac	ttttcagaaa	aaccatgtct	1250
tttatgctat	aatcattcca	aattttgcca	gtgttaagtt	acaaatgtgg	1300
tgtcattcca	tgttcagcag	agtattttta	ttatattttc	tcgggattat	1350
tgctcttctg	tctataaatt	ttgaatgata	ctgtgcctta	attggttttc	1400
atagttttaag	tgtgtatcat	tatcaaagtt	gattaatttg	gottcatagt	1450
ataatgagag	cagggctatt	gtagttccca	gattcaatcc	accgaagtgt	1500
tactgtcat	ctgttaggga	atTTTTgttt	gtcctgtctt	tgccctggatc	1550
catagcgaga	gtgctctgta	TTTTTTTTta	gataatttgt	atTTTTgcac	1600
actgagatat	aataaaaaggt	gtttatcata	aaaaaaaaaa	aaaaaaaa	1648

 $\langle 210 \rangle$ 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
1				5					10					15	
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
 cttcgcgatc ttccgcgtta cttcttctgct ggcgttggtg ggagccgtgc 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200
 tttgcatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctcttggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccott ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tggtcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tgggtacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca ttttaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1				5					10					15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
				20					25					30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
				35					40					45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
				50					55					60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
				65					70					75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
				80					85					90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
				95					100					105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn
				110					115					120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
				125					130					135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu

Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser	140	145	150
				155					160					165			
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val			
				170					175					180			
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln			
				185					190					195			
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu			
				200					205					210			
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu			
				215					220					225			
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys			
				230					235					240			
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser			
				245					250					255			
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser			
				260					265					270			
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys			
				275					280					285			
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys			
				290					295					300			
Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val			
				305					310					315			
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu			
				320					325					330			
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln			
				335					340					345			
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg			
				350					355					360			
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro			
				365					370					375			
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp			
				380					385					390			
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly			
				395					400					405			
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr			
				410					415					420			
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val			
				425					430					435			

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50
 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100
 tcagggcttg tgccctctcg cttcctgacg ctccctggcg atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcactgt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtaccct gggcctcttt gcagtggagc tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgc ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
 agctgtcaact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgtttttagt taacattaag acttatatac agtttttagg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	
				50					55					60	
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	
				65					70					75	
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	
				80					85					90	
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	
				95					100					105	
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	
				110					115					120	
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	
				125					130					135	
Lys	Lys	Lys	Pro	Phe											
				140											

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200

```

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
tcccggaacc tgccgccctg ccactatgtc ccgccgctct atgctgcttg 50
cctgggctct cccagcctc cttcgactcg gagcggctca ggagacagaa 100
gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200
tatgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggttgaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450
ccaggccatc cgggcagccc agggcttact ggctgcggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccgga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc cctgaggcc ctgctgatcc gcacccatt cctcccctcc 650
catggc aaa aaccocactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

```

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
1 5 10 15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
tctatctggt catctgtggc caggatgatg gtcctcccgg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200

gcggggccac atctcaccta agtcccggcc catggccaat tccactctcc 250
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac aggggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
cacttccaac acaatgccac agggcaggga aacatctcca tcagcctcgt 500
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg 650
ctcccagagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700
tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggctg 750
gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
cccatctggg tgaccggggg caggccacag agggcaggcc agggctggaa 850
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900
gttgggcctc aggcaggag ggggggtggag acgaggagat gccaagtggg 950
gccagggccca agtctcaagt ggcagagaaa ggggtccaag tgctggtccc 1000
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100
ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
atggatggct gagagggtt cctaggagcc agtcagcagg gtgggggtggg 1300
gccagaggag ctctccagcc ctgcctagt ggcgccctga gcccttgtc 1350
gtgtgctgag catggcatga ggctgaagt gcaaccctgg ggtctttgat 1400
gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500
cccatcctta agctaagaca ggacgattgt ggtcctccca cactaaggcc 1550
acagcccac cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg 1600
ctcctctggg agcatccatg tcccggagag gggtcctca acagtcagcc 1650

tcacctgtca gaccgggggtt ctcccggatc tggatggcgc cgccctctca 1700
gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750
tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
1 5 10 15

Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
20 25 30

Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
35 40 45

Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
50 55 60

Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
65 70 75

Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
80 85 90

Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
95 100 105

Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
110 115 120

Asn Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
125 130 135

His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
140 145 150

Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
155 160 165

Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
170 175 180

Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
185 190 195

Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50
gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100
gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
gcgcgcgcgc cgccgtcgct cctgcagcgc tgtcgacctg gccgctagca 250
tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
gcgccagcc ggctgcggct gcccacacgg ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcggtgc cggccgtgct gctggctctc acgctgccgg 400
ggctgcccgct ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgca ctgcaaccog gccacggact ccaagggctc 500
ctcttctctc ccgctgggga tatcggtccg ggcggccaac tccaaggtcg 550
ctcttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
tgttactcgt gaagctgccg cgaatgggtg cctgctctac ctagataaag 850
aggataaggt ttacctaaaa ctggagaaag gtaatttggt tggaggctgg 900
cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
 aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
 acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
 gaattttatt tgttttagttt taaaagactg gcaaccaggt ctaaggatta 1300
 gaaaactcta aagttctgac ttcaatcaac ggtagtggtg atactgccaa 1350
 agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400
 ggaattagtt tgtttgggtt ttgtaaaaaa cttggatttt ttttttcagt 1450
 aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgcccac 1500
 aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
 gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600
 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650
 aaagtgtctt acccaaaatc taagtgtctc atccctgagc ctgagcaaaa 1700
 cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750
 aatgattgat aataaccact ttattaaaaa cctaagggtt tttttttttc 1800
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900
 tgccttaact ctttaaattg tatatatatta tctgttttagc taatattaaa 1950
 ttcaaataatc ccatatctaa atttagtgc atattctgtc ttttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
1				5					10					15

Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
			20						25					30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
			35						40					45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50					55					60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala		65	70	75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr		80	85	90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe		95	100	105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr		110	115	120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile		125	130	135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe		140	145	150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val		155	160	165
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu		170	175	180
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly		185	190	195
Phe	Leu	Val	Phe	Pro	Leu											200		

<210> 221

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 221

acggctcacc atgggctccg 20

<210> 222

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 222

aggaagagga gcccttggag tccg 24

<210> 223

<211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgctgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactotta aaaaaagcca 300
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350
ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
gtcattatct tgctgcatgt attctggggc attgtatatt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
tggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

```
Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
  1           5           10           15

Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
          20           25           30

Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
          35           40           45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
          50           55           60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
          65           70           75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
          80           85           90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
          95           100          105

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
          110          115          120

Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
          125          130          135

Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
          140          145          150

Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
          155          160          165

Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
          170          175          180

Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
          185          190          195

His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
          200          205          210

Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
          215          220          225

Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
          230          235          240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
          245          250          255

Ser Arg
```

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

```
cggaaccag cgcgcgcac caccgctgcc actgccgcc tgccggggcc 50
atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100
gagccatctg ggggttctgg ggcccaagaa cgtctcgag aaagacgccg 150
agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacaccttca accatactgt gaccgcgaac aggacagagg gcgtgcgtgt 250
gtctgtgaac gtcctgaaca agcagaaggg ggcgccgttg ctgtttgtgg 300
tccgccagaa ggaggctgtg gtgtccttcc aggtgcccct aatcctgcga 350
gggatgtttc agcgcaagta cctctaccaa aaagtgaac gaaccctgtg 400
tcagcccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450
tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550
agcagcacag cccagctact tcaagtatga gttccctgaa ggcgtggact 600
cggtaatgtg caaggcgacc tccaacaagg ccttcccctg ctcagtcac 650
tccattcagg atgtgctgtg tcctgtctat gacctggaca acaacgtagc 700
cttcatcggc atgtaccaga cgatgaccaa gaaggcggcc atcaccgtac 750
agcgcaaaga cttcccagc aacagctttt atgtggtggt ggtggtgaag 800
accgaagacc aagcctgagg gggctccctg cttttctacc ctttcgcaga 850
agatgaaccg gtgatcaag ggcaccgcca gaaaaccctg tcagtgtgtg 900
tgttcaagc agtcacgtct gaggcatagc tcagtgggat gctcttttgc 950
ctgggtatat ttctctcctt ttacctgtg accgtcctcc tggcctgtg 1000
ggagaactgg aggcagaaga agaagaccct gctggtggcc attgaccgag 1050
cctgccaga aagcggtcac cctcgagtcc tggctgattc ttttcctggc 1100
agttccccct atgaggggta caactatggc tcctttgaga atgtttctgg 1150
atctaccgat ggtctggttg acagcgctgg cactggggac ctctcttacg 1200
gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250
tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300
ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350
```


tggcacggaa ggacaagcgt gttctgcgga aaaagtacca gatctacttc 1400
 tggaacattg ccaccattgc tgtcttctat gcccttcctg tggcgcagct 1450
 ggtgatcacc taccagacgg tggatgaatgt cacagggaat caggacatct 1500
 gctactacaa cttcctctgc gccacccac tgggcaatct cagcgccttc 1550
 aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttct 1600
 gctcatcatc ctgcaacggg agatcaacca caaccgggcc ctgctgcgca 1650
 atgacctctg tgccctggaa tgtgggatcc ccaaactt tgggcttttc 1700
 tacgccatgg gcacagccct gatgatggag gggctgctca gtgcttgcta 1750
 tcatgtgtgc cccaactata ccaatttcca gtttgacaca tcgttcatgt 1800
 acatgatcgc cggactctgc atgctgaagc tctaccagaa gcggcaccgc 1850
 gacatcaacg ccagcgccta cagtgcctac gcctgcctgg ccattgtcat 1900
 cttcttctct gtgctggggc tggctcttgg caaagggaac acggcgcttc 1950
 ggatcgtctt ctccatcatt cacatcatcg ccacctgct cctcagcacg 2000
 cagctctatt acatgggccc gtggaaactg gactcgggga tcttcgccc 2050
 catcctccac gtgctctaca cagactgcat ccggcagtgc agcgggccc 2100
 tctacgtgga ccgcatgggt ctgctggtca tgggcaacgt catcaactgg 2150
 tcgctggctg cctatgggct tatcatgcgc ccaatgatt tcgcttccta 2200
 cttgttgccc attggcatct gcaacctgct cctttacttc gccttctaca 2250
 tcatcatgaa gctccggagt ggggagagga tcaagctcat cccctgctc 2300
 tgcacgttt gcacctccgt ggtctggggc ttgcgctct tcttcttctt 2350
 ccagggaactc agcacctggc agaaaacccc tgcagagtcg agggagcaca 2400
 accgggactg catcctctc gaactctttg acgaccacga catctggcac 2450
 ttctctctc ccatcgccat gttcgggtcc ttctggtgt tgctgacact 2500
 ggatgacgac ctggatactg tgcagcggga caagatctat gtcttctagc 2550
 aggagctggg cccttcgctt cacctcaagg ggcctgagc tcctttgtgt 2600
 catagaccgg tcaactctgtc gtgctgtggg gatgagtccc agcaccgtg 2650
 cccagcactg gatggcagca ggacagccag gtctagctta ggcttggcct 2700
 gggacagcca tggggtggca tggaacctg cagctgccct ctgccgagga 2750
 gcaggcctgc tcccctggaa ccccagatg ttggccaaat tgctgctttc 2800

ttctcagtgt tggggccttc catgggcccc tgtcctttgg ctctccattt 2850
 gtccctttgc aagaggaagg atggaaggga caccctcccc atttcatgcc 2900
 ttgcattttg ccggtcctcc tccccacaat gcccagcct gggacctaag 2950
 gcctcttttt cctccatac tcccactcca gggcctagtc tggggcctga 3000
 atctctgtcc tgtatcaggg cccagttct ctttgggctg tccctggctg 3050
 ccatcactgc ccattccagt cagccaggat ggatgggggt atgagatttt 3100
 gggggttggc cagctgggtgc cagacttttg gtgctaaggc ctgcaagggg 3150
 cctggggcag tgcgtattct cttccctctg acctgtgctc agggctggct 3200
 ctttagcaat gcgctcagcc caatttgaga accgccttct gattcaagag 3250
 gctgaattca gaggtcacct cttcatccca tcagctccca gactgatgcc 3300
 agcaccagga ctggaggag aagcgcctca ccccttcct tccttctttc 3350
 caggccctta gtcttgccaa accccagctg gtggcctttc agtgccattg 3400
 acactgcccc agaatgtcca ggggcaaagg agggatgata cagagttcag 3450
 ccggttctgc ctccacagct gtgggcaccc cagtgcctac cttagaaagg 3500
 ggcttcagga agggatgtgc tgtttcctc tacgtgcccc gtcctagcct 3550
 cgctctagga cccagggtg gcttctaagt ttccgtccag tcttcaggca 3600
 agttctgtgt tagtcatgca cacacatacc tatgaaacct tggagtttac 3650
 aaagaattgc cccagctctg ggcaccctgg ccaccctggc ccttggatcc 3700
 ccttcgtccc acctggtcca cccagatgc tgaggatggg ggagctcagg 3750
 cggggcctct gctttgggga tgggaatgtg tttttctccc aaactgttt 3800
 ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850
 tcagagcgtc tccatgctat ggttgcatth ccgttttcta tgaatgaatt 3900
 tgcattcaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
1				5					10					15

Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

	320		325		330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala	335		340		345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly	350		355		360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser	365		370		375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe	380		385		390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	395		400		405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys	410		415		420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala	425		430		435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe	440		445		450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val	455		460		465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn	470		475		480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly	485		490		495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile	500		505		510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile	515		520		525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu	530		535		540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr	545		550		555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys	560		565		570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met	575		580		585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro	590		595		600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile	605		610		615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
				620					625					630	
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
				815					820					825	
Arg	Asp	Lys	Ile	Tyr	Val	Phe									
				830											

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

```

gctcaagtgc cctgccttgc cccacccagc ccagcctggc cagagccccc 50
tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc 100
ttgggcgctg gagggcctgt cctgaccatg gtcctgcct ggctgtggct 150
gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

```

tgtctgtgga agttccagaa aactatggtg gaaatttccc tttataacctg 250
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350
 ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag 400
 taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg 450
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550
 ggcatcccct tcctcttctc tgaggcttca gaccgggatg agccaggcac 600
 agccaactcg gatcttcgat tccacatcct gagccaggct ccagcccagc 650
 cttccccaga catgttccag ctggagcctc ggctgggggc tctggccctc 700
 agccccaagg ggagcaccag ccttgaccac gccctggaga ggacctacca 750
 gctgttggtg caggtcaagg acatgggtga ccaggcctca ggccaccagg 800
 ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850
 gagcctatcc acctggcaga gaatctcaaa gtcctatacc cgcaccacat 900
 ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc 950
 atcccccgga accctttgaa gtgaatgcag agggaaacct ctacgtgacc 1000
 agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc 1050
 tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100
 tgggtgatga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150
 tacagtcagca tccctgagct cagtccacca ggtactgaag tgactagact 1200
 gtcagcagag gatgcagatg cccccggctc ccccaattcc cacgttgtgt 1250
 atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300
 caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tccactccg 1350
 agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400
 cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450
 atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500
 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550
 ttgatgctga cctcgagccc gccttcgcc tcatggattt tgccattgag 1600
 aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg 1650

gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctccaa 1700
 gtcattgagg ggtggtggtg gtgcagagtg tggcgaagct ggtggggcca 1750
 ggcccaggcc ctggagccac cgccacggtg actgtgctag tggagagagt 1800
 gatgccaccc cccaagttag accaggagag ctacgaggcc agtgtcccca 1850
 tcagtgtccc agccggtctt ttctgtctga ccatccagcc ctccgacccc 1900
 atcagccgaa ccctcagggt ctccctagtc aatgactcag agggctggct 1950
 ctgcattgag aaattctccg gggagggtgca caccgcccag tccctgcagg 2000
 gcgcccagcc tggggacacc tacacggtgc ttgtggaggc ccaggataca 2050
 gccctgactc ttgcccctgt gccctcccaa tacctctgca caccgcca 2100
 agaccatggc ttgatcgtga gtggaccag caaggacccc gatctggcca 2150
 gtgggcacgg tccctacagc ttcacccttg gtccaaccc cacggtgcaa 2200
 cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt 2250
 ggccctgcat tgggtggagc cacgtgaaca cataatcccc gtggtggtca 2300
 gccacaatgc ccagatgtgg cagctcctgg ttgagtgat cgtgtgtcgc 2350
 tgcaacgtgg aggggcagtg catgcgcaag gtgggccgca tgaaggcat 2400
 gccacgaag ctgtcggcag tgggcatact ttaggcacc ctggtagcaa 2450
 taggaatctt cctcatctc attttcacc actggaccat gtcaaggag 2500
 aaggaccgg atcaaccagc agacagcgtg ccctgaagg cgactgtctg 2550
 aatggcccag gcagctctag ctgggagctt ggcctctggc tccatctgag 2600
 tccctggga gagagcccag caccgaagat ccagcagggg acaggacaga 2650
 gtagaagccc ctccatctgc cctggggtgg aggcaccatc accatcacca 2700
 ggcattgtct cagagcctgg acaccaactt tatggactgc ccatgggagt 2750
 gctccaaatg tcagggtgtt tgccaataa taaagcccca gagaactggg 2800
 ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848

<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
1					5				10					15

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

	20	25	30
Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro	35	40	45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp	50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser	65	70	75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala	80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val	95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn	110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu	125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala	140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe	155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe	170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly	185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu	200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala	215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser	230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro	245	250	255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr	260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu	275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala	290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp	305	310	315

1000
900
800
700
600
500
400
300
200
100
0

	605	610	615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp
	620	625	630
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu
	635	640	645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His
	650	655	660
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser
	665	670	675
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val
	680	685	690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr
	695	700	705
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile
	710	715	720
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val
	725	730	735
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg
	740	745	750
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val
	755	760	765
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile
	770	775	780
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp
	785	790	795
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val	
	800	805	

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgcccttaccg cgcagcccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequeunce

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50
atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttcctgag 250
atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550
ttcccagagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650
atggatattt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700
tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750
gctcctgcat tgggtctgac ccaaatagaa actggaacgc tagttttgca 800
ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggaccca 850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
 atgggaatth caagggcttc atcgacctgc acagctactc gcagctgctg 950
 atgtatccat atgggtactc agtcaaaaag gcccagatg ccgaggaact 1000
 cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050
 ctgagtacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100
 agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150
 tgagttgaga gataccggga cctatggctt cctcctgcca gctaaccaga 1200
 tcatccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250
 catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300
 atttgtaccc acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350
 cctacctgtg tgagtcagag ccctctgggt ttgtggagca cacaggcctg 1400
 cccctctcca gccagctccc tggagtcgtg tgtcctggcg gtgtccctgc 1450
 aagaactggt tctgccagcc tgcctcaattt tggctctgct gtttttgatg 1500
 agccttttgt ctgtttctcc ttccacctg ctggctgggc ggctgcactc 1550
 agcatcacc cttcctgggt ggcatgtctc tctctacctc atttttagaa 1600
 ccaaagaaca totgagatga ttctctaccc tcatccacat ctagccaagc 1650
 cagtgcactt gctctgggtg cactgtggga gacaccactt gtcttttagt 1700
 gggctctcaa gatgatgtag aatttccttt aatttctcgc agtcttcctg 1750
 gaaaatatth tcttttgagc agcaaactct gtagggatat cagtgaagg 1800
 ctctccctcc ctcctctcct gttttttttt tttttgagac agagttttgc 1850
 tcttgttgcc caggctggag tgtgatggct cgatcttggc tcaccacaac 1900
 ctctgcctcc tgggttcaag caattctcct gcctcagcct cttgagtagc 1950
 ttggtttata ggcgcctgac accatgcctg gctaattttg tgtttttagt 2000
 agagacaggg tttctocatg ttggctcaggc tggctctcaa ctcccaacct 2050
 caggatgatc gccctccttg gcctcccaga gtgctgggat tacagggtgtg 2100
 agccactgtg ccgggcccgt cccctccttt ttaggcctg aatacaaaagt 2150
 agaagatcac tttccttcac tgtgctgaga atttctagat actacagttc 2200
 ttactcctct cttccctttg ttattcagtg tgaccaggat ggcgggaggg 2250
 gatctgtgtc actgtaggta ctgtgccag gaaggctggg tgaagtgacc 2300

atctaaattg caggatgggtg aaattatccc catctgtcct aatgggctta 2350
 cctcctcttt gccttttgaa ctcaattcaa agatctagga ctcatcttac 2400
 aggtcctaaa tcactcatct ggcttgata atctcactgc cctggcacat 2450
 tcccatttgt gctgtgggtg atcctgtgtt tccttgtcct ggtttgtgtg 2500
 tgtgtgtgtg tgtgtgtgtg tgtgtgtgtt tgtgtgtgtg tgtctgtcta 2550
 ttttgtatcc tggaccacaa gttcctaagt agagcaagaa ttcataacc 2600
 agctgcctct tgtttcatct cacctcagca cgtaccatct gtccttttgt 2650
 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700
 tcttaacotc ctgcctagga tttgtacagc atctgggtgtg tgcttataag 2750
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
1				5					10					15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

<400> 235

caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50
tgttccaaaa tggcatctta cttttatgga gtactctttg ctgttggcct 100
ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150
cccgcccttc ctccacaaag agcácccctg cctcacaggt gtattccctc 200
aacaccgact ttgccttcog cctataccgc aggctggttt tggagacccc 250
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300
tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggtt 400
ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgacctga 450
agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaa 500
ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550
tttctccaac ccctccattg ccaggcgag gatcaacagc catgtgaaaa 600
agaagacca aggaaggtt gtagacataa tccaaggcct tgaccttctg 650
acggccatgg ttctggtgaa tcacattttc tttaaagcca agtgggagaa 700
gccctttcac cttgaatata caagaaagaa cttccattc ctggtgggcg 750
agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800
tttggggtgg atacagagct gaactgcttt gtgctgcaga tggattacaa 850
gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900
aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950
ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000
ctcctacaat ctggaaacca tcctcccgaa gatgggcatc caaaatgcct 1050
ttgacaaaaa tgctgatttt tctggaattg caaagagaga ctccctgcag 1100
gtttctaaag caaccacaa ggctgtgctg gatgtcagt aagagggcac 1150
tgaggccaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200
gtccctctta cttcactgtc tccttcaata ggaccttcct gatgatgatt 1250
acaaataaag ccacagacgg tattctcttt ctagggaaag tggaaaatcc 1300
cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350
tgcacaagaa ataacaaacc acatccctct ttctgttctg aggtgcatt 1400
tgaccccagt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

aatcaccaaa ccatcaacag ggaccccagt cacaagccaa caccattaa 1500
 cccagtcag tgcccttttc cacaaattct ccagggtaac tagcttcacg 1550
 ggatgttgct gggttacat atttcattc cttggggctc ccaggaatgg 1600
 aaatagcca acccaggtta ggcacctcta ttgcagaatt acaataacac 1650
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1 5 10 15

Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30

Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45

Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60

Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75

Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90

Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105

Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120

Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135

Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150

Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165

Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180

Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195

Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

	200	205	210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe
	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met
	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn
	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe
	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala
	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys
	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser
	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala
	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser
	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser
	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile
	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn
	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile
	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	
	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100
 gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
 ggacccaggc atottgcttt ccagccacaa agagacagat gaagatgcag 250
 aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300
 aacaaattcc aatgagacta gcacctctgc caaacttgga tccagtgtga 350
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
 agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
 gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
 gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600
 caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650
 ctgggtccag tgtgacctcc agtggagcca gcaactgccac caactctgag 700
 tccagcacag tgtccagttag ggccagcact gccaccaact ctgagtctag 750
 cacactctcc agtggggcca gcacagccac caactctgac tccagcaca 800
 cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850
 agtggggcca gcacagccac caactctgag tccagcacag tgtccagttag 900
 ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950
 gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000
 gccaccaact ctgagtccag cagcacctcc agtggggcca gcacagccac 1050
 caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100
 ctgagtccag cagcacctcc agtggggcca gcacagccac caactctgag 1150
 tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200
 cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250
 tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacaccctcc 1300
 agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350
 ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400
 gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450
 gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

caactctgac tccagcacia cctccagtga ggccagcaca gccaccaact 1550
ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag 1600
tccagcacia cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650
tgtgacctct gcaggctctg gaacagcagc tctgactgga atgcacacia 1700
cttcccatag tgcattctact gcagtgagtg aggcaaagcc tgggtgggtcc 1750
ctgggtgccgt gggaaatctt cctcatcacc ctggtctcgg ttgtggcggc 1800
cgtgggggtc tttgctgggc tcttctctctg tgtgagaaac agcctgtccc 1850
tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaacat 1900
ggccttggtc caggccctgg agggaatcat ggagcccccc acaggcccag 1950
gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000
agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050
gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt 2100
cattcatccc aggagacccc tccagcttt gtttgagatc ctgaaaatct 2150
tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300
gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5				10						15
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
			20					25						30
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
			35					40						45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
			50					55						60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
			65					70						75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				335					340					345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				350					355					360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala		
380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala		
395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala		
410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala		
425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val		
440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala		
455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala		
470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala		
485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile		
500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe		
515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn		
530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly		
545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro		
560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile		
575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro		
590	595	

<210> 244
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccagacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tggggtcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctgggggcctc 750
 agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
 tttctgaaat ccctgaaggg gggtgtactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccgggccg gcctggcaag ggggacgagt 50
cagtggacac tccaggaaga gcggccccgc ggggggcat gaccgtgcgc 100
tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcgacc gcggggcgga gctgcgcgcc gtgagtcgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgtcc tgctctccga atgctgcga 250
ccgcgatggg cctgaggagc tggtcgcgc ccccatgggg cgcgtgcgc 300
cctcgccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350
gccgcctccg acctgggcgc tcagcccccg gatcagcctg cctctgggct 400
ctgaagagcg gccattcctc agattcgaag ctgaacacat ctccaactac 450
acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500
agaggccctc tttgcaactc gtagcaacct cagcttcctg ccaggcgggg 550
agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc 600
agcttcaagg gcaaggacc acagcgcgac tgtcaaaact acatcaagat 650
cctcctgcgc ctacgggca gtcacctgtt cacctgtggc acagcagcct 700
tcagcccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750
gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800
cgaccogaat ttcaagtcca ctgccctggg ggtgatggc gagctctaca 850
ctggaacagt cagcagcttc caagggaatg acccgccat ctgcggagc 900
caaagccttc gcccaccaa gaccgagagc tccctcaact ggctgcaaga 950
cccagctttt gtggcctcag cctacattcc tgagagcctg ggcagcttgc 1000
aaggcgatga tgacaagatc tactttttct tcagcgagac tggccaggaa 1050
tttgagttct ttgagaacac cattgtgtcc cgcattgcc gcactctcaa 1100
ggcgatgag ggtggagagc ggtgctaca gcagcgtgg aactccttc 1150
tcaaggcca gctgctgtgc tcacggccc acgatggctt ccccttcaac 1200
gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250
cacccttttc tatgggtct tacttccca gtggcacagg ggaactacag 1300
aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350
agcggcctct acaaggaggt gaaccgtgag acacagcagt ggtacaccgt 1400
gaccacccg gtgccacac cccggcctgg agcgtgcatc accaacagt 1450

80

85

90

Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr
95 100 105

Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys
110 115 120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile
125 130 135

Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly
140 145 150

Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn
155 160 165

Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp
170 175 180

Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala
185 190 195

Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe
200 205 210

Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro
215 220 225

Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
230 235 240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly
245 250 255

Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu
260 265 270

Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile
275 280 285

Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp
290 295 300

Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp
305 310 315

Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro
320 325 330

Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr
335 340 345

Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val
350 355 360

Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys
365 370 375

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

	665		670		675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro		
	680		685		690
Val Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys		
	695		700		705
Ala Ser Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val		
	710		715		720
Met Cys Thr Leu	Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe		
	725		730		735
Leu Leu Tyr Arg	His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln		
	740		745		750
Gly Glu Cys Ala	Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu		
	755		760		765
Pro Pro Glu Thr	Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser	Thr		
	770		775		780
Pro Leu Asp His	Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro	Pro		
	785		790		795
Gly Ala Arg Val	Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser	Ile		
	800		805		810
Gln Asp Ser Phe	Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg		
	815		820		825
Val Arg Leu Gly	Ser Glu Ile Arg Asp	Ser Val Val			
	830		835		

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 254
 agcccggtgca gaatctgctc ctgg 24

 <210> 255
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtoct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
ctaagccgga ggatgtgcag ctgcggcggc ggcgcgggct acgaagagga 50
cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100
agggcgggac gggagcccgg actcgtctgc cgccgcgctc gtcgccgtcg 150

aaggatgatca gtgtttgcct ttgaacacat cttcttgctg aacattatgt 3100
agcagacctg cttaactttg acttgaaatg tacctgatga acaaaacttt 3150
tttaaaaaaa tgttttcttt tgagaccctt tgctccagtc ctatggcaga 3200
aaacgtgaac attcctgcaa agtattattg taacaaaaca ctgtaactct 3250
ggtaaatgtt ctgttgatgat tgttaacatt ccacagattc taccttttgt 3300
gttttgtttt ttttttttac aattgtttta aagccatttc atgttccagt 3350
tgtaagataa ggaaatgtga taatagctgt ttcattcattg tottcaggag 3400
agctttccag agttgatcat ttcctctcat ggtactctgc tcagcatggc 3450
cacgtagggtt ttttgtttgt tttgttttgt tctttttttg agacggagtc 3500
tcactctgtt acccaggctg gaatgcagtg gcgcaatctt ggctcacttt 3550
aacctccact tccctgggtc aagcaattcc cctgcctttg cctcccgagt 3600
agctgggatt acaggcacac accaccacgc ccagntagtt tttttgtatt 3650
tttagtagag acgggggttc accatgcaag cccagctggc cacgtagggtt 3700
ttaaagcaag gggcgtgaag aaggcacagt gaggtatgtg gctgttctcg 3750
tggtagtcca ttcggcctaa atagacctgg cattaaattt caagaaggat 3800
ttggcatttt ctcttcttga cccttctctt taaagggtaa aatattaatg 3850
tttagaatga caaagatgaa ttattacaat aaatctgatg tacacagact 3900
gaaacataca cacatacacc ctaatcaaaa cggtggggaa aaatgtattt 3950
ggttttgttc ctttcatcct gtctgtgtta tgtgggtgga gatggttttc 4000
attctttcat tactgttttg ttttatcctt tgtatctgaa ataccttta 4050
tttatttaat atctgttggt cagagctctg ccatttcttg agtacctgtt 4100
agttagtatt atttatgtgt atcgggagtg tgtttagtct gttttatttg 4150
cagtaaaccg atctccaaag atttcctttt ggaaacgctt tttcccctcc 4200
ttaattttta tattccttac tgttttacta aatattaagt gttctttgac 4250
aattttggtg ctcatgtgtt ttggggacaa aagtgaaatg aatctgtcat 4300
tataccagaa agttaaattc tcagatcaaa tgtgccttaa taaatttggt 4350
ttcattttaga tttcaaacag tgatagactt gccattttaa tacacgtcat 4400
tggagggctg cgtatttgta aatagcctga tgctcatttg gaaaaataaa 4450
ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500

attcctgttt tagctgaaga attgtattac atttggagag taataaaactt 4550

aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
1 5 10 15

Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	245	250	255
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	260	265	270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	275	280	285
Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala	290	295	300
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu	305	310	315
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg	320	325	330
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser	335	340	345
Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro	350	355	360
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu	365	370	375
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly	380	385	390
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu	395	400	405
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala	410	415	420
Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly	425	430	435
Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp	440	445	450
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val	455	460	465
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile	470	475	480
Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys	485	490	495
Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser	500	505	510
Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu	515	520	525
His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu			

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe Glu	
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val Leu	
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu Glu	
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe Cys	
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile Phe	
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro Ser	
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg Asn	
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu Asp	
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr Phe	
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu Met	
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn Asn	
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50
tgacaccttc cctttcggcc ttgaggttcc cagcctggtg gccccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtag gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccatttc 500
 tggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaac 600
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650
 ccatatgtta cctcatataa gtcacctgtc accacttttag ataagagcac 700
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750
 aaactgcatg agaaaaaacc gaagagtttg gaaagcacc agagagtttg 800
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtga 850
 acaggcactt cttagtgaac ccagcaacc agcatataga gaagatattg 900
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150
 tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200
 aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300
 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350
 atgtgttatg aacaattttc atatgcacta aaaaccta ataaaaataa 1400
 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15
Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser

50										55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys					
				65					70					75					
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
				80					85					90					
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
				95					100					105					
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115					120					
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130					135					
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145					150					
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160					165					
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175					180					
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190					195					
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys					
				200					205					210					
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220					225					
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235					240					
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250					255					
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265					270					
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280					285					
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295					300					
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310					315					
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325					330					
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
				335					340					345					

Leu Leu Lys Val Tyr
350

<210> 266
<211> 2403
<212> DNA
<213> Homo sapiens

<400> 266
cggctcgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag 50
acagctggcc tgacctcaa atcatccatc caccctgct gtcactgtt 100
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcactg 200
gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250
tgctccctct ttctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tgggtccacct ctacagagat ggggaagact 350
gggaatctaa gcagatgcca cagtatcgag ggagaactga gtttgtgaag 400
gactccattg caggggggcg tgtctctcta aggctaaaaa acatcactcc 450
ctcggacatc ggctgtatg ggtgctggtt cagttcccag atttacgatg 500
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550
atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc 600
ctcaggctgg ttccccagc ccacagccaa gtggaaaggt ccacaaggac 650
aggatttgtc ttcagactcc agagcaaagc cagatgggta cagcctgtat 700
gatgtggaga tctccattat agtcaggaa aatgctggga gcatattgtg 750
ttccatccac ctgctgagc agagtcatga ggtggaatcc aaggatttga 800
taggagagac gtttttccag ccctcacctt ggcgcctggc ttctatttta 850
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000
gtgactctgg atccagagac ggctcaccgc aagctctgcg tttctgatct 1050
gaaaactgta acccatagaa aagctcccca ggagggtgct cactctgaga 1100
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaagcaggg 1150
agacattact gggagggtga cgtgggacaa aatgtagggt ggtatgtggg 1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300
acattcaatc cccattttat cagcctcccc cccagcacc ctcctacacg 1350
agtaggggtc ttcctggact atgaggggtg gaccatctcc ttcttcaata 1400
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
ttgttgagac cctatatcca gcatgcatg tatgacgagg aaaaggggac 1500
tcccatattc atatgtccag tgcctgggg atgagacaga gaagacacctg 1550
cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc 1600
ccgacaggtg gccccagctt cctctccgga gcctgcgcac agagagtcac 1650
gccccccact ctcctttagg gagctgaggt tcttctgccc tgagccctgc 1700
agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750
gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800
ttagggtttag tttgtgaaaa ctocatccag ctaagcgatc ttgaacaagt 1850
cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggtt 1950
tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000
accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050
aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
gtccatatcc ctcattaaca cagacacaaa aattctaaat aaaattttta 2250
caaattaaac taaacaatat atttaaagat gatataatac tactcagtgt 2300
ggtttgtccc acaaatgcag agttggttta atatttaa atcaaccagt 2350
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
aaa 2403

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
1				5				10					15	

Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320					325					330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val
				335					340					345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp
				350					355					360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn
				365					370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr
				380					385					390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr
				395					400					405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe
				410					415					420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
				425					430					435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr
				440					445					450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp
				455					460					465
Gly														

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
 ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg 50
 tggtgagggc taggaaaaga gtttggttggg aaccctgggt tatcggcctc 100
 gtcattctca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct cagggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggacccct aaagtagatc 500

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
 Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
 1 5 10 15
 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20 25 30
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	
				230					235					240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	
				245					250					255	
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	
				260					265					270	
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	
				275					280					285	
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	
				290					295					300	
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	
				305					310					315	
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	
				320					325					330	
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	
				335					340					345	
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	
				350					355					360	
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	
				365					370					375	
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	
				380					385					390	
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	
				395					400					405	
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	
				410					415					420	
Thr	Gly	Ile													

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
 gtcgaagggtt ataaaagctt ccagccaaac ggcattgaag ttgaagatac 50
 aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100
 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
 80 85 90
 Val Arg Ile Ala Ala Glu Gly Arg Ala Val Val His Trp Cys
 95 100 105
 Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
 110 115 120
 Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
 125 130 135
 Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
 140 145 150
 Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
 155 160 165
 Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
 170 175 180
 Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
 185 190 195
 Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
 200 205 210
 Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
 215 220 225
 Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
 230 235

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
 agagaaagaa gcgtctccag ctgaagccaa tgcagccctc cggtctctccg 50
 cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatc 100
 cccaggcggg cgtggggcac cgggccagc gccgacgac gctgccgttt 150
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
 gotcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
 acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300
 tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
 aacgagggta gaggaagcag tcattttgac ttactttcct gtgggttcac 400
 cggtcattgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
atgaacagga acttatgggt ccagtagaat ggtcagatat ggtcactttg 600
aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650
tgcttggaaat ttttttcaga gagagtttaa gtgctgtgga gtagtatatt 700
tcaactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050
agcctgtcaa gaatctttga acacacatcc atggcaaaca gotttaatac 1100
acacttttag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150
caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgcttataaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaa atgctgaaga cagatgtcat 1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450
atgggtgggac tggagccata gtaaagggtg atttacttct accaactagt 1500
atataaagta ctaattaaat gctaacatag gaagttagaa aataactaata 1550
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat 1600
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc 1700
tgatcagggg ttttttgat ataagtctgt gttaaatotg tataattcag 1750
tcgatttcag ttctgataat gttaagaata accattatga aaaggaaaat 1800
ttgtcctgta tagcatcatt attttttagcc tttcctgtta ataaagcttt 1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000
 cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
 ctcttttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100
 aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150
 ttcttttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
 tttagagatt ctttgtttta tttcaactgat taatatactg tggcaaatta 2250
 cacagattat taaatttttt tacaagagta tagtatattt atttgaaatg 2300
 ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350
 atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
 1 5 10 15

Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
 20 25 30

Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45

Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60

Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75

Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90

Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105

Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120

Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135

Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150

Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165

Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

	170		175		180
Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His	Gln		
	185		190		195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met		
	200		205		210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe		
	215		220		225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu		
	230		235		240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu	Pro		
	245		250		255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His		
	260		265		270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg		
	275		280		285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His	Phe		
	290		295		300
Glu Met Glu Glu	Leu				
	305				

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
 gagagaggca gcagcttgct cagcggacaa ggatgctggg cgtgagggac 50
 caaggcctgc cctgcactcg ggcctcctcc agccagtgtc gaccagggac 100
 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgtctgc 150
 cttggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
 agagccagca tggtacagga tcctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
 cgggcagcct ctccacttca tcccaggagaa gcagctgtgt gacggagagc 450
 tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550
 ggtgctggac tcggccacag ggaactgggt ctctgcctgt ttcgacaact 600

tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650
gctgtggaga ttggcccaga ccaggatctg gatgttggtg aaatcacaga 700
aaacagccag gagcttcgca tgcggaactc aagtggggccc tgtctctcag 750
gctccctggt ctccctgcac tgtcttgctt gtgggaagag cctgaagacc 800
ccccgtgtgg tgggtgggga ggaggcctct gtggattctt ggccttggca 850
ggtcagcatc cagtacgaca aacagcaagt ctgtggaggg agcatcctgg 900
acccccactg ggtcctcagc gcagcccact gcttcaggaa acataccgat 950
gtgttcaact ggaaggtgag ggcaggctca gacaaactgg gcagcttccc 1000
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050
ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100
tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150
tccagccacc ccactctgga tcattggatg gggctttacg aagcagaatg 1200
gaggggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccaggggtg 1350
acagtgggtg gcccctgatg taccaatctg accagtggca tgtggtgggc 1400
atcgttagct ggggctatgg ctgcgggggc ccgagcacc caggagtata 1450
caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500
agctgtaatg ctgctgcccc ttgacagtgc tgggagccgc ttcttctctg 1550
ccctgcccac ctgggggatcc cccaaagtca gacacagagc aagagtcccc 1600
ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650
ggcctcaatt cctgtaagag accctgcag cccagaggcg cccagaggaa 1700
gtcagcagcc ctagctcggc cacacttggg gctcccagca tcccaggag 1750
agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccagaagg 1800
aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
tcttcaccca tcccgaagcc tactagagca agaaaccagt tgtaataata 1950
aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000
gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	
				260					265					270	
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	
				275					280					285	
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	
				290					295					300	
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	
				305					310					315	
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	
				320					325					330	
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	
				335					340					345	
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	
				350					355					360	
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	
				365					370					375	
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	
				380					385					390	
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	
				395					400					405	
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	
				410					415					420	
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu				
				425					430						

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
 gggctgagggc actgagagac cggaaagcct ggcattocag agggagggaa 50
 acgcagcggc atccccaggc tccagagctc cctggtgaca gtctgtggct 100
 gagcatggcc ctcccagccc tgggcctgga cccctggagc ctectgggcc 150
 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc agggggcccat gccaggggtc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctocag gattttgaca 300
 ctctgctcct gagtggtgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctgggt 500
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
tgcttgtacc ttcatgaac ttcaagattc ctacctgttg cccatctcgg 600
aggacaaggt catggaggga aaaggccaaa gccccttga ccccgctcac 650
aagcatacgg ctgtcttggg ggatgggatg ctctattctg gtactatgaa 700
caacttcctg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
ctgtcctcaa gaccgacaac ttctcctcgt ggctgcatca tgacgcctcc 800
tttgtggcag ccatcccttc gaccaggtc gtctacttct tcttcgagga 850
gacagccagc gagtttgact tctttgagag gctccacaca tcgoggggtg 900
ctagagtctg caagaatgac gtggggggcg aaaagctgct gcagaagaag 950
tggaccacct tcctgaaggc ccagctgctc tgcaccagc cggggcagct 1000
gcccttcaac gtcatccgcc acggggtcct gctccccgcc gattctccca 1050
cagctcccca catctacgca gtcttcacct cccagtggca ggttggcggg 1100
accaggagct ctgcggtttg tgcttctct ctcttgga ttgaacgtgt 1150
ctttaagggg aaatacaaag agttgaacaa agaaacttca cgctggacta 1200
cttatagggg ccctgagacc aacccccggc caggcagttg ctcagtgggc 1250
ccctcctctg ataaggccct gaccttcatt aaggaccatt tctgatgga 1300
tgagcaagtg gtggggagcg ccctgctggt gaaatctggc gtggagtata 1350
cacggcttgc agtgagagca gccaggggcc ttgatgggca cagccatctt 1400
gtcatgtacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450
tggggacagc agtgctcatc tgggtggaaga gattcagctg ttccctgacc 1500
ctgaacctgt tcgcaacctg cagctggccc ccaccagggt tgcagtgttt 1550
gtaggcttct caggaggtgt ctggagggtg ccccgagcca actgtagtgt 1600
ctatgagagc tgtgtggact gtgtccttgc ccgggacccc cactgtgcct 1650
gggacctga gtcccgaacc tgttgcttcc tgtctgcccc caacctgaac 1700
tcctggaagc aggacatgga gcgggggaac ccagagtggg catgtgccag 1750
tgggcccatg agcaggagcc ttcggcctca gagccgcccg caaatcatta 1800
aagaagtcct ggctgtcccc aactccatcc tggagctccc ctgccccac 1850

ctgtcagcct tggcctctta ttattggagt catggcccag cagcagtccc 1900
 agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
 atggagttgg ggggtctctac cagtgtctgg caactgagaa tggcttttca 2000
 taccctgtga tctcctactg ggtggacagc caggaccaga ccctggccct 2050
 ggatcctgaa ctggcaggca tccccggga gcatgtgaag gtcccgttga 2100
 ccagggtcag tgggtggggc gccctggctg ccagcagtc ctactggccc 2150
 cactttgtca ctgtcactgt cctctttgcc ttagtgcttt caggagccct 2200
 catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250
 ttcagggctg tgagaccctg cgccctgggg agaaggcccc gttaagcaga 2300
 gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350
 ggacgctgac aacaactgcc taggcactga ggtagcttaa actctaggca 2400
 caggccgggg ctgcggtgca ggcacctggc catgctggct gggcgggcca 2450
 agcacagccc tgactaggat gacagcagca caaaagacca cttttctccc 2500
 ctgagaggag cttctgctac tctgcatcac tgatgacact cagcaggggtg 2550
 atgcacagca gtctgcctcc cctatgggac tcccttctac caagcacatg 2600
 agctctctaa caggggtggg gctaccccca gacctgctcc tacactgata 2650
 ttgaagaacc tggagaggat ccttcagttc tggccattcc agggaccctc 2700
 cagaaacaca gtgtttcaag agaccctaaa aaacctgcct gtcccaggac 2750
 cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcca 2800
 ctcttgaaa ctccactctg aagctgcgcg tttggacacc aacactccct 2850
 tctcccaggg tcatgcaggg atctgctccc tctgcttcc cttaccagtc 2900
 gtgcaocgct gactcccagg aagtotttcc tgaagtctga ccacotttct 2950
 tcttgcttca gttggggcag actctgatcc cttctgccct ggcagaatgg 3000
 caggggtaat ctgagccttc ttcactcctt taccctagct gacccttca 3050
 cctctcccc tcccttttcc tttgttttgg gattcagaaa actgcttgtc 3100
 agagactgtt tttttttat taaaaatata aggcttaaaa aaa 3143

<210> 277
 <211> 761
 <212> PRT
 <213> Homo sapiens
 <400> 277

Met 1	Ala	Leu	Pro	Ala 5	Leu	Gly	Leu	Asp	Pro 10	Trp	Ser	Leu	Leu	Gly 15
Leu	Phe	Leu	Phe	Gln 20	Leu	Leu	Gln	Leu	Leu 25	Leu	Pro	Thr	Thr	Thr 30
Ala	Gly	Gly	Gly	Gly 35	Gln	Gly	Pro	Met	Pro 40	Arg	Val	Arg	Tyr	Tyr 45
Ala	Gly	Asp	Glu	Arg 50	Arg	Ala	Leu	Ser	Phe 55	Phe	His	Gln	Lys	Gly 60
Leu	Gln	Asp	Phe	Asp 65	Thr	Leu	Leu	Leu	Ser 70	Gly	Asp	Gly	Asn	Thr 75
Leu	Tyr	Val	Gly	Ala 80	Arg	Glu	Ala	Ile	Leu 85	Ala	Leu	Asp	Ile	Gln 90
Asp	Pro	Gly	Val	Pro 95	Arg	Leu	Lys	Asn	Met 100	Ile	Pro	Trp	Pro	Ala 105
Ser	Asp	Arg	Lys	Lys 110	Ser	Glu	Cys	Ala	Phe 115	Lys	Lys	Lys	Ser	Asn 120
Glu	Thr	Gln	Cys	Phe 125	Asn	Phe	Ile	Arg	Val 130	Leu	Val	Ser	Tyr	Asn 135
Val	Thr	His	Leu	Tyr 140	Thr	Cys	Gly	Thr	Phe 145	Ala	Phe	Ser	Pro	Ala 150
Cys	Thr	Phe	Ile	Glu 155	Leu	Gln	Asp	Ser	Tyr 160	Leu	Leu	Pro	Ile	Ser 165
Glu	Asp	Lys	Val	Met 170	Glu	Gly	Lys	Gly	Gln 175	Ser	Pro	Phe	Asp	Pro 180
Ala	His	Lys	His	Thr 185	Ala	Val	Leu	Val	Asp 190	Gly	Met	Leu	Tyr	Ser 195
Gly	Thr	Met	Asn	Asn 200	Phe	Leu	Gly	Ser	Glu 205	Pro	Ile	Leu	Met	Arg 210
Thr	Leu	Gly	Ser	Gln 215	Pro	Val	Leu	Lys	Thr 220	Asp	Asn	Phe	Leu	Arg 225
Trp	Leu	His	His	Asp 230	Ala	Ser	Phe	Val	Ala 235	Ala	Ile	Pro	Ser	Thr 240
Gln	Val	Val	Tyr	Phe 245	Phe	Phe	Glu	Glu	Thr 250	Ala	Ser	Glu	Phe	Asp 255
Phe	Phe	Glu	Arg	Leu 260	His	Thr	Ser	Arg	Val 265	Ala	Arg	Val	Cys	Lys 270
Asn	Asp	Val	Gly	Gly 275	Glu	Lys	Leu	Leu	Gln 280	Lys	Lys	Trp	Thr	Thr 285
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro

290 295 300

Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	305	310	315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	320	325	330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	335	340	345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	350	355	360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	365	370	375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	380	385	390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	395	400	405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	410	415	420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	425	430	435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	440	445	450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	455	460	465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	470	475	480
Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	485	490	495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	500	505	510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	515	520	525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	530	535	540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	545	550	555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	560	565	570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	575	580	585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtogetcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
aggggtccctt agccggggcgc agggcgcgca gccaggctg agatccgcgg 50
cttccgtaga agtgagcatg gctgggcagc gagtgtttct tctagtgggc 100
ttcctttctcc ctgggggtcct gctctcagag gctgccaaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gttttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgtttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaattgagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcatcggc tctttggaat ttgggctacc 600
aatccccctg tcttatgttc cagtattccg ttccttgctg actgatcaca 650
tggaacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800
agttgtgggt cattaaactct gactttgcct ttgattttgc tcgacctctg 850
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttgagaa acttcattgc caagtttggg gactctgggt 950
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100
 atgtgaaaat tgtggactgg cttcctcaga gtgacctcct ggctcaccca 1150
 agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200
 catccagcat ggtgtgcca tgggtgggat ccctctcttt ggagaccagc 1250
 ctgaaaacat ggtccgagta gaagccaaaa agtttgggtgt ttctattcag 1300
 ttaaagaagc tcaaggcaga gacattggct cttaatgaat aacaaatcat 1350
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcacctcgc 1400
 gctccacccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450
 gtcctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500
 gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550
 tcaactctggg gactctatgg ctttgtggga agctgctggg catggctgtc 1600
 tgggtggctgc gtggggccag aaaggtgaag gagacataag gccagggtgca 1650
 gccttggcgg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700
 cccactagtt ctggcagccc cattctctag tccttctagt tatctcctgt 1750
 tttcttgaag aacaggaaaa atggccaaaa atcatccttt ccacttgcta 1800
 attttgctac aaattcatcc ttactagctc ctgcctgcta gcagaaatct 1850
 ttccagtcct cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900
 gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950
 aaaatccacc ttcttctca tgcgcctctc cgaatcacac cctgactctt 2000
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100
 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150
 tgtgcttgag agttcagggc cggacacagg ctacacaggtc tccacattgg 2200
 gtccctgtct ctggtgcca cagtgaagct cttcttgggt gagcaggcat 2250
 ggagactgta gggttccaga tttcctgaaa aataaaagtt tacagcgta 2300
 tctctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1				5					10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
 ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
 cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150
 gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
 cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
 gttcagcgag cctagagagg gcagactatc aggggtgccgg cggtgagaat 400
 ccaggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgacaga gccctcagc catgttggga gccaaagccac actggctacc 500
 aggtcccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550
 tgggggcccgg gtggggccag gaggggtcag agcccgctct gctggagggg 600
 gagtgcctgg tgggtctgtga gcctggccga gctgctgcag gggggcccgg 650
 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcgacca ggtcctgggt aacgagggcg gtggctttga 800
 ccgggcctct ggctccttcg tagccctgt ccggggtgtc tacagcttcc 850
 ggttccatgt ggtgaagggt tacaaccgcc aaactgtcca ggtgagcctg 900
 atgctgaaca cgtggcctgt catctcagcc ttggccaatg atcctgacgt 950
 gacccgggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150
 cccagaaac agcagaggca ggagagagac tccctctggc tcctatocca 1200
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250
 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300
 ccctcccagc cacctgctgc atctgttcct gcctgcagcc ctaggatcag 1350
 ggcaagggtt ggcaagaagg aagatctgca ctactttgg gcctctgctc 1400
 ctccggttcc cccaccccag cttcctgctc aatgctgac agggacaggt 1450
 ggcgcagggt agcctgacag gccccacag gagcccagat ggacaagcct 1500
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctagggtggg 1600
 aggctcagcc acaggcagaa ggggtgggaag ggcttgaggt ctgtggctgg 1650
 tgaggaagga aggaggggtg attgtctaga ctgaacatgg tacacattct 1700
 gcatgtatag cagagcagcc agcaggtagc aatcctgggt gtccttctat 1750
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800
 tgagtgtgtt tgctctgggt gagagcagag ctgagagcag gtatacagag 1850
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
 cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050
 gctgtcttat tctcctcctt aggcttccta ttacctggga ttccatgatt 2100
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150
 tcttatcccg ctgtccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatggtgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 287
 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
 1 5 10 15
 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
 20 25 30
 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn
 80 85 90
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu
 95 100 105
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val
 110 115 120
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn
 125 130 135
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val
 140 145 150
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
 155 160 165
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

170	175	180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser		
185	190	195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu		
200	205	

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccagggtgtcc 50
 tagccgccca gcctcgacgc cgtcccgga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttccccgagg gcggtgactg ggccgggcttc agccatgaag accctcatag 200
 ccgcctactc cgggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctacaggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
 tcacctgggt caataggtcc aaggtggaaa agcagctaca ggtcatctca 400
 gtgctccagt ggggtcctgtc cttccttgta ctgggagtgg cctgcagtgc 450
 catcctcatg tacatattct gcaactgatt ctgggtcatc gctgtgctct 500
 acttcaactg gctgggtgttt gactggaaca cacccaagaa aggtggcagg 550
 aggtcacagt ggggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650
 atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700
 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750
 gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800
 agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850
 tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtgggtcg 900
 ggggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950
 tgcggaaccg caagggcttt gtgaaactgg ccctgcgtca tggagctgac 1000
 ctgggttcca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050
 ottcgaggag ggctcctggg gccgatgggt ccagaagaag ttccagaaat 1100
 acattggttt cgcctccatg atcttccatg gtcgaggcct cttctcctcc 1150
 gacacctggg ggctgggtgcc ctactccaag cccatcacca ctgttggtgg 1200
 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
 acctgtacca caccatgtac atggaggccc tgggtgaagct cttcgacaag 1300
 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350
 agccagcctt cggggccaat tccttgagg aaccagctgc aaatcacttt 1400
 tttgctctgt aaatttgaa gtgtcatggg tgtctgtggg ttatttataa 1450
 gaaattataa caattttgct aaacaaaaa aaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaa aaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1				5					10					15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50
ccgacgcagg gccggggccgg gccagggcc gaggagcgcg gcggccagag 100
cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggccgtg 250
caccgcgtcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctotacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggtcctg cacggagtgt aactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gtcceaaggc cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcggc tggacgtggt actttctgga gattgtgttc 700
tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggtgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800
ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850
gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
atgtaaccct gaacttcaga ggaaacaaga acccgccctt gctggggatc 1000
ctctacggga agaagtacga ggcgacatg tgcgtgagga gatttcctct 1050
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcattg 1150

tttccagggg agcagtttaa gcctgcccg aggccgtgga ccctcctgaa 1200
 cttcctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250
 tgggcgtctt tgccagcgga tcacctctcc tgatcctgac tttcttgggg 1300
 tttgtgggag cagcttcctt tggagtgcgc agactgatag gagaatcgct 1350
 tgaacctggg aggtggagat tgcagtgagc tgagatggca tcactgtact 1400
 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaaca 1450
 aaaaaccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500
 attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550
 agcttgaaga tggtagcttg agatctttca ggctaataaa aaaagaatga 1600
 aggaaaatta acagcctcag agacctatgg tgcaccgtca cacaataca 1650
 catatgcatg atgagagtcc cagaaggaga ggagagaaaag ggtcagaaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150
 ggggtcaggc tgatctcaaa ctctgagtt caggatgatc gccgcctca 2200
 gcctcccaa gtgttgatg tgcaggcgtg agccactgcg cctggccgga 2250
 atttcttttt aaggctgaat gatgggggcc aggcacgatg gctcacgcct 2300
 gtgatcccaa gtagcttgga ttgtaaacat gcaccaccat gcctggctaa 2350
 tttttgtatt ttagtagag acgtgttagc caggctggtc tcgatctcct 2400
 gacctcaagt gaccacctgc ctacagcctc caaagtactg ggattacagg 2450
 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550
 cctttttaaa tttttattat ttatttatat atttattttg agacagggtc 2600

ttgttctgtt gccaggctg gactacagtg gcacagtctt ggctcaactgc 2650
 agcctcgacc tcctgggctg cagtgatcct ccacactcag cctcccttgt 2700
 agctgtatatt ttttgtatatt tgtattttgt agctgtagtt tttgtatattt 2750
 ttgtggagac agcatttcac catgatgccc aggctgggtct tgaactcctg 2800
 agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacta 2950
 ccaggagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000
 cagtgaagtcg aggttgtgag actgcattcc agcctggaca acagagtgag 3050
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 298
 cttcctctgt gggtggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt attttaaga atctgaagta ctatgcatca ctccctccaa 50

tgctctgggg cagccaccag gcatattcat ctttgttgt gtitttcttt 100

tgcttttagca ctggggcact tcttgcttat ttctttgga ggaaaggggc 150

tcagtttgct ttgtggggtt ggtggcaggc aggcgggctt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctggggt ctgagacctg ctctctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450

tgctggttct gtaatgtgt atgcatggg gtctttgcac aagcctttcc 500

tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

atgtagtcac cctgcagatt tcaattctaa catcattttc tccagggatc 600

ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650

ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700

gttgatatgg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctoa gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gcccagggttg ggcattctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcacttttg gaggctgagg caggctgac 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggttg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5				10						15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65				70						75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80				85						90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95				100						105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110				115						120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125				130						135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgctgg agcagtggcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500
 ggcgatggct cccactggcc aggcacagc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaa 800
 gtggcagggg aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgctctcat cagccaggca gcagcaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc 1100
 ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattggc tcagtgttgg ccaggaggt 1200
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250

tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tggttcaa at gatctccaag ggcccttata cccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat 1450
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccct gtcttacta aaaatacaaa aaaactagcc 1600
 aggcattgtg gtgtgtgcct gtatccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatggtt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

gcggggccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50
 tgtcactgcc tcccgccgcc tctgtcccgc gccatgaccc agccggtgcc 100
 ccggctctcc gtgcccgcgc cgctggccct gggctcagcc gcactgggcg 150
 ccgccttcgc cactggcctc ttctgtggga ggcggtgccc cccatggcga 200
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250
 gtatctttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350
 caggcccagc tcttggccaa cctggcgcgg ctcatccagg ccaagaaggc 400
 gctggacctg ggcaccttca cgggctactc cgccctggcc ctggccctgg 450
 cgctgccgcg ggacggggcg gtggtgacct gcgaggtgga cgcgcagccc 500
 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550
 cgacctccgg ctgaagcccg ccttgagac cctggacgag ctgctggcgg 600
 cgggcgaggc cggcaccttc gacgtggcgc tgggtgatgc ggacaaggag 650
 aactgctccg cctactacga gcgctgcctg cagctgctgc gaccggagg 700
 catectcgcc gtcctcagag tctgtggcg cgggaagggtg ctgcaacctc 750
 cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcac 800
 cggcgggacg tcaggttcta catcagcctc ctgccctgg gcgatggact 850
 caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1				5					10					15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
ccgccgcgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50
ctctcgccgt cagcatgcc aacgccttca agcccgggga cttggtgttc 100
gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150
ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt ccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
 agggctgtgg gagatccaga acaaccccc aagcagctac agcgcccctc 350
 cgccagttag ctctccgac agcgaggccc cagaggcaa ccccgccgac 400
 ggcagttagc ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
 agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550
 aagatgtcgg tctcgaaacg agcccgaag gcctccagcg acctggatca 600
 ggccagcgtg tccccatccg aagaggagaa ctcggaagc tcatctgagt 650
 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
 cgggcgccac ggagggggccc tctgggggga cggaaaaaa agaaggcgcc 750
 gtcagcctcc gactccgact ccaaggccga ttccgacggg gccaaagcctg 800
 agcgggtggc catggcgagg tggggtcct cctcctctc ttctcctcc 850
 tcctccgact ccgatgtgtc tgtgaagaag cctccgagg gcaggaagcc 900
 agcggagaag cctctcccga agccgcgagg gcggaaaccg aagcctgaac 950
 ggctccgctc cagctccagc agtgacagt acagcgacga ggtggaccgc 1000
 atcagttagt ggaagcgggc ggacgaggcg cggaggcgcg agctggaggc 1050
 ccggcgggcg cgagagcagg aggaggagct gcggcgccct cgggagcagg 1100
 agaaggagga gaaggagcg aggcgcgagc gggccgaccg cggggaggct 1150
 gagcggggca gcggcggcag cagcggggac gagctcaggg aggacgatga 1200
 gcccgtaag aagcggggac gcaaggcccg gggccggggt ccccgctcct 1250
 cctctgactc cgagcccag gccgagctgg agagagagg caagaaatca 1300
 gcgaagaagc cgcagtcctc aagcacagag cccgccagga aacctggcca 1350
 gaaggagaag agagtgcggc ccgaggagaa gcaacaagc aagcccgtga 1400
 aggtggagcg gacccggaag cggccgagg gcttctcgat ggacaggaag 1450
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500
 cagttagatc aagtttgccc taaaggctga cagcccggac gtgaagaggt 1550
 gcctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600
 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcccggtta 1650
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tataccggc 1700

tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750
aaggtctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800
gctggccggg gaggaggccc ccaggagaa ggcggaggac aagcccagca 1850
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900
agcgcagagg acaaggagca cgaggagggg cgggactcgg aggagggggc 1950
aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000
acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050
gactcggagg ccctggacga ggagagctga gccgcgggca gccaggccca 2100
gcccccgccc gagctcaggc tgcccctctc cttccccggc tcgcaggaga 2150
gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttcctt 2200
gggttttttt ttctgccta atttctgtga tttccaacca acatgaaatg 2250
actataaacg gttttttaat ga 2272

<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
1				5					10					15
Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

	140		145		150
Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser		
	155		160		165
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala		
	170		175		180
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu		
	185		190		195
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala		
	200		205		210
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys		
	215		220		225
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser		
	230		235		240
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser		
	245		250		255
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val		
	260		265		270
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro		
	275		280		285
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser		
	290		295		300
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu		
	305		310		315
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg		
	320		325		330
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln		
	335		340		345
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly		
	350		355		360
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp-Glu Leu	Arg		
	365		370		375
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly		
	380		385		390
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu		
	395		400		405
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser		
	410		415		420
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg		
	425		430		435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
440 445 450
Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
455 460 465
Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
470 475 480
Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
485 490 495
Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
500 505 510
Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
515 520 525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
530 535 540
Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
545 550 555
Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
560 565 570
Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
575 580 585
Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
590 595 600
Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
605 610 615
Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
620 625 630
Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
635 640 645
Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
650 655 660
Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser
665 670

<210> 309
<211> 3871
<212> DNA
<213> Homo sapiens

<400> 309
gttggttctc ctggatcttc accttaccaa ctgcagatct tgggactcat 50
cagcctcaat aattatatta aattaacacc atttgaaaga gaacattggt 100

ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150
 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250
 taaaagact tgctgctttc aaatagctgt attccotttt tgggttcac 300
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350
 tgctcttggg agccaaagac cacatctttc tactcagtct ggttgactta 400
 aacaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450
 attatgtaaa ttagctggga aagatgccaa tacagaatgt gcaaatttca 500
 tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550
 ggagcatttc atccaatatg tgggtatatt gatcttgag tctacaagga 600
 ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650
 aatgtccttt cgatcctcag cagccttttg cttcagtaat gacagatgag 700
 tacctctact ctggaacagc ttctgatttc cttggcaaag atactgcatt 750
 cactcgatcc cttgggccta ctcatgacca ccactacatc agaactgaca 800
 tttcagagca ctactggctc aatggagcaa aatttattgg aactttcttc 850
 ataccagaca cctacaatcc agatgatgat aaaatatatt tcttctttcg 900
 tgaatcatct caagaaggca gtacctccga taaaaccatc ctttctcgag 950
 ttggaagagt ttgtaagaat gatgtaggag gacaacgcag cctgataaac 1000
 aagtggacga cttttcttaa ggccagactg atttgctcaa ttcctggaag 1050
 tgatggggca gatacttact ttgatgagct tcaagatatt tatttactcc 1100
 ccacaagaga tgaaagaaat cctgtagtat atggagtctt tactacaacc 1150
 agctccatct tcaaaggctc tgctgtttgt gtgtatagca tggctgacat 1200
 cagagcagtt tttaatggc catatgctca taaggaaagt gcagaccatc 1250
 gttgggtgca gtatgatggg agaattcctt atccacggcc tggtagatgt 1300
 ccaagcaaaa cctatgaccc actgattaag tccaccogag attttccaga 1350
 tgatgtcatc agtttcataa agcggcactc tgtgatgtat aagtccgtat 1400
 acccagttgc aggaggacca acgttcaaga gaatcaatgt ggattacaga 1450
 ctgacacaga tagtggtgga tcatgtcatt gcagaagatg gccagtacga 1500
 tgtaatgttt cttggaacag acattggaac tgtcctcaaa gttgtcagca 1550

tttcaaagga aaagtggaat atggaagagg tagtgctgga ggagttgcag 1600
atattcaagc actcatcaat catcttgaac atggaattgt ctctgaagca 1650
gcaacaattg tacattgggt cccgagatgg attagttcag ctctccttgc 1700
acagatgcga cacttatggg aaagcttgcg cagactgttg tcttgccaga 1750
gaccctact gtgcctggga tggaaatgca tgctctcgat atgctcctac 1800
ttctaaaagg agagctagac gccaaagatgt aaaatatggc gacccaatca 1850
cccagtgtcg ggacatcgaa gacagcatta gtcatgaaac tgctgatgaa 1900
aaggtgattt ttggcattga atttaactca acctttctgg aatgtatacc 1950
taaatcccaa caagcaacta ttaaattggt tatccagagg tcaggggatg 2000
agcatcgaga ggagttgaag cccgatgaaa gaatcatcaa aacggaatat 2050
gggctactga ttcgaagttt gcagaagaag gattctggga tgtattactg 2100
caaagcccag gagcacactt tcatccacac catagtgaag ctgactttga 2150
atgtcattga gaatgaacag atggaaaata cccagagggc agagcatgag 2200
gaggggcagg tcaaggatct attggctgag tcacggttga gatacaaaga 2250
ctacatccaa atccttagca gccc aaactt cagcctcgac cagtactgcg 2300
aacagatgtg gcacagggag aagcggagac agagaaacaa gggggggcca 2350
aagtggaagc acatgcagga aatgaagaag aaacgaaatc gaagacatca 2400
cagagacctg gatgagctcc ctagagctgt agccacgtag ttttctactt 2450
aatttaaaga aaagaattcc ttacctataa aaacattgcc ttctgttttg 2500
tatatccctt atagtaattc ataaatgctt cccatggagt tttgctaagg 2550
cacaagacaa taatctgaat aagacaatat gtgatgaata taagaaaggg 2600
caaaaaattc atttgaacca gttttccaag aacaaatctt gcacaagcaa 2650
agtataagaa ttatcctaaa aatagggggg ttacagttgt aaatgtttta 2700
tgttttgagt tttggaattt attgtcatgt aaatagttga gctaagcaag 2750
ccccgaattt gatagtgtat aaggtgcttt attccctcga atgtccatta 2800
agcatggaat ttacatgca gttgtgctat gttcttatga acagatatat 2850
cattcctatt gagaaccagc taccttgtgg tagggaataa gaggtcagac 2900
acaaattaag acaactccca ttatcaacag gaactttctc agtgagccat 2950
tcactcctgg agaattggtat aggaatttgg agaggtgcat tatttctttc 3000

tggccactgg gggttaaattt agtgtactac aacattgatt tactgaaggg 3050
 cactaatgtt tccccagga tttctattga ctatgcagga gtaacagggt 3100
 cacagagaga agttgggtgct tagttatgtg ttttttagag tatatactaa 3150
 gctctacagg gacagaatgc ttaataaata ctttaataag atatgggaaa 3200
 atattttaat aaaacaagga aaacataatg atgtataatg catcctgatg 3250
 ggaaggcatg cagatgggat ttgttagaag acagaaggaa agacagccat 3300
 aaattctggc tttggggaaa actcatatcc ccatgaaaag gaagaacaat 3350
 cacaaataaa gtgagagtaa tgtaatggag ctcttttcac tagggataaa 3400
 gtagctgcc aatttgtaatt catctgttaa aaaaaatcta gattataaca 3450
 aactgctagc aaaatctgag gaaacataaa ttcttctgaa gaatcatagg 3500
 aagagtagac attttattta taaccaatga tatttcagta tatattttct 3550
 ctcttttaaa aaatatattat catactctgt atattatttc tttttactgc 3600
 ctttattctc tcctgtatat tggattttgt gattatattt gagtgaatag 3650
 gagaaaacaa tatataacac acagagaatt aagaaaatga catttctggg 3700
 gagtggggat atatatttgt tgaataacag aacgagtgt aaattttaac 3750
 aacggaaagg gttaaattaa ctctttgaca tcttactca accttttctc 3800
 attgctgagt taatctgttg taattgtagt attgtttttg taatttaaca 3850
 ataaataagc ctgctacatg t 3871

<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

Met	Asn	Ala	Asn	Lys	Asp	Glu	Arg	Leu	Lys	Ala	Arg	Ser	Gln	Asp
1				5					10					15
Phe	His	Leu	Phe	Pro	Ala	Leu	Met	Met	Leu	Ser	Met	Thr	Met	Leu
				20					25					30
Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45
Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
				50					55					60
Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75
Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile

				80					85					90
Phe	Leu	Leu	Ser	Leu 95	Val	Asp	Leu	Asn	Lys 100	Asn	Phe	Lys	Lys	Ile 105
Tyr	Trp	Pro	Ala	Ala 110	Lys	Glu	Arg	Val	Glu 115	Leu	Cys	Lys	Leu	Ala 120
Gly	Lys	Asp	Ala	Asn 125	Thr	Glu	Cys	Ala	Asn 130	Phe	Ile	Arg	Val	Leu 135
Gln	Pro	Tyr	Asn	Lys 140	Thr	His	Ile	Tyr	Val 145	Cys	Gly	Thr	Gly	Ala 150
Phe	His	Pro	Ile	Cys 155	Gly	Tyr	Ile	Asp	Leu 160	Gly	Val	Tyr	Lys	Glu 165
Asp	Ile	Ile	Phe	Lys 170	Leu	Asp	Thr	His	Asn 175	Leu	Glu	Ser	Gly	Arg 180
Leu	Lys	Cys	Pro	Phe 185	Asp	Pro	Gln	Gln	Pro 190	Phe	Ala	Ser	Val	Met 195
Thr	Asp	Glu	Tyr	Leu 200	Tyr	Ser	Gly	Thr	Ala 205	Ser	Asp	Phe	Leu	Gly 210
Lys	Asp	Thr	Ala	Phe 215	Thr	Arg	Ser	Leu	Gly 220	Pro	Thr	His	Asp	His 225
His	Tyr	Ile	Arg	Thr 230	Asp	Ile	Ser	Glu	His 235	Tyr	Trp	Leu	Asn	Gly 240
Ala	Lys	Phe	Ile	Gly 245	Thr	Phe	Phe	Ile	Pro 250	Asp	Thr	Tyr	Asn	Pro 255
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Arg 265	Glu	Ser	Ser	Gln	Glu 270
Gly	Ser	Thr	Ser	Asp 275	Lys	Thr	Ile	Leu	Ser 280	Arg	Val	Gly	Arg	Val 285
Cys	Lys	Asn	Asp	Val 290	Gly	Gly	Gln	Arg	Ser 295	Leu	Ile	Asn	Lys	Trp 300
Thr	Thr	Phe	Leu	Lys 305	Ala	Arg	Leu	Ile	Cys 310	Ser	Ile	Pro	Gly	Ser 315
Asp	Gly	Ala	Asp	Thr 320	Tyr	Phe	Asp	Glu	Leu 325	Gln	Asp	Ile	Tyr	Leu 330
Leu	Pro	Thr	Arg	Asp 335	Glu	Arg	Asn	Pro	Val 340	Val	Tyr	Gly	Val	Phe 345
Thr	Thr	Thr	Ser	Ser 350	Ile	Phe	Lys	Gly	Ser 355	Ala	Val	Cys	Val	Tyr 360
Ser	Met	Ala	Asp	Ile 365	Arg	Ala	Val	Phe	Asn 370	Gly	Pro	Tyr	Ala	His 375

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
380 385 390

Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro
395 400 405

Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe
410 415 420

Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
425 430 435

Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
440 445 450

Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
455 460 465

Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
470 475 480

Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
485 490 495

Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
500 505 510

Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly
515 520 525

Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala
530 535 540

Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
545 550 555

Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
560 565 570

Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
575 580 585

Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
590 595 600

Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
605 610 615

Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
620 625 630

Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
635 640 645

Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
650 655 660

Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

<400> 313
ggccagactg atttgctcaa ttcctggaag tgatggggca gatac 45

<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

ccctgacctc cctgagccac actgagctgg aagccgcaga ggtcatcctg 50
gagcatgccc accgcgggga gcagacaacc tcccaggtaa gctgggagca 100
agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150
ctcagcagtt tcagccagca gggactgatc aggtgtgtgt cctggagtgg 200
ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250
cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300
gggtgaggtg ggggggcaca ggtgtcatgt gcaccttctt gtctcagcaa 350
gaagagctga gagaggggat cttggagcca ttgaggggtg catggagcta 400
cagaggggag ggaaaggtat ttttaagtaa cagtgtggca caatagttaa 450
gagcacagtt tttggagcta gaccgacata ggttcaaatt ctcttctgtt 500
gcttcctagt tctgtagccc caggtaaggg agtgacttaa cctctctgga 550
cttcaatttc ctcatcacta aagtagggcc aataatagca cccacctcat 600
aggggaagatt aaatgacata atgtatgtga tgcaactagc aaagtaccag 650
tcccatagta agtcatgccc cacagtattt ccacccaccc ctgttctctg 700
ccttcccaac caggtactgc aacgactgga gcagaggcgg cagcaggctt 750
cagagcggga ggctccaagc atagaacaga gggttacagga agtgcgagag 800
agcatccgcc gggcacaggt gagccaggtg aagggggctg ccoggctggc 850
cctgctgcag ggggctggct tagatgtgga gcgctggctg aagccagcca 900
tgaccacaggc ccaggatgag gtggagcagg agcggcggct cagtgaggct 950
cggctgtccc agagggacct ctctccaacc gctgaggatg ctgagctttc 1000
tgactttgag gaatgtgagg agacgggaga gctctttgag gaggctgccc 1050
cccaagccct ggccacgagg gccctcccct gccctgcaca cgtgggtattt 1100
cgctatcagg cagggcgtag ggatgagctg acaatcacgg agggtagtg 1150
gctggaggtc atagaggagg gagatgctga cgaatgggtc aaggctcgga 1200
accagcacgg cgaggtaggc tttgtccctg agcgatatct caacttcccg 1250

gacctctccc tcccagagag cagccaagac agtgacaatc cctgcggggc 1300
 agagcccaca gcattcctgg cacaggccct gtacagctac accggacaga 1350
 gtgcagagga gctgagcttc cctgaggggg cactcatccg tctgctgccc 1400
 cgggcccacg atggagtaga tgacggcttc tggaggggag aatttggggg 1450
 cagtgttggg gtcttccctt ccctgctggt ggaagagctg cttggccccc 1500
 cagggccacc tgaactctct gaccctgaac agatgctgcc gtccccttct 1550
 cctcccagct tctcccacc tgcacctacc tctgtgttgg atgggcccc 1600
 tgcacctgtc ctgcctgggg acaaagccct ggacttcctt gggttcctgg 1650
 acatgatggc acctcgactc aggccgatgc gtccaccacc tccccgccc 1700
 gctaaagccc cggatcctgg ccaccagat cccctcacct gaaggccagg 1750
 gaagccttga ccccagtgga tgctgctgtc cctatcttca agctgtcaga 1800
 ccacaccatc aatgatccag agcaacacag ccaaaagctg gaatcgccct 1850
 tatttccacc ctcacctcca agggtggaag cttgcccctt cccatttcta 1900
 gagctggaac ccactccttt ttttccatt gttctatcat ctctaggacc 1950
 ggaactacta ccttctcttc tgtcatgacc ctatctaggg tggtgaaatg 2000
 cctgaaatct ctggggctgg aaaccatcca tcaaggtctc tagtagttct 2050
 ggcccacctc tttcccacc ctggctccat gaccacccc actctggatg 2100
 ccagggtcac tgggggttgg ctggggagag gaacaggcct tgggaatcag 2150
 gagctggagc caggatgcga agcagctgta atggctctgag cggatttatt 2200
 gacaatgaat aaagggcacg aaggccaggc cagggcctgg gcctcttgtg 2250
 ctaagagggc agggggccta cgggtctatt gctttagggg cccaccacgg 2300
 gcaggggcct gctcccagct gccacgctct atcatatgga gcgaggtggt 2350
 ggggaaggcg gggcaggcag cctgttgtag gcaggggaag gagaagagac 2400
 tgaggggctg tgacctctcc tgaggcccc agcctgagac tgtgcaactc 2450
 cagggtggaag tagagctggt ccctcagctg gggggcagtg ctgtccagtg 2500
 gaggggaggg ctttcacgcc caccacccc ctggccctgc cagctggtag 2550
 tccatcagca caatgaagga gacttgaga agaggaagaa taactactgtt 2600
 gcttctgtt caagctgtgt ccagctttt ccctggggct ccaggacctt 2650
 ccctacctcc accaccaaac caagggattt atagcaaagg ctaagcctgc 2700

agtttactct ggggggttcag ggagccgaaa ggcttaaata gtttaagtag 2750
 gtgatgggaa gatgagatta cctcatttag ggctcaggca gactcacctc 2800
 acatactccc tgctccctgt ggtagagaca cctgagagaa aggggagggg 2850
 tcaacaatga gagaccagga gtaggtccta tcagtgcctc ccagagtaga 2900
 gagcaataag agcccagccc agtgcagtcc cggctgtgtt ttctacctg 2950
 gtgatcagaa gtgtctgggt tgcttggtg cccatttgcc tcttgagtgg 3000
 gcagccctgg gcttggggcc ctccctccgg ccctcagtgt tggctctgca 3050
 gaagctctgg ggttcccttc aagtgcacga ggggttaggc tgctgtccct 3100
 gagtcccca ttctgtactg gggggctggc taggacctgg ggctgtggcc 3150
 tctcaggggg cagcctctcc atggcaggca tccctgcctt gggctgccct 3200
 cccccagacc cctgaccacc ccctgggtcc tgtccccac cagagcccca 3250
 gctcctgtct gtgggggagc catcacgtg ttcgtgcagt ccatagcgct 3300
 tctcaatgtg tgtcacccgg aacctgggag gggagggaac actggggttt 3350
 aggaccacaa ctgagaggct gcttggccct cccctctgac caggacatc 3400
 ctgagtttgg tggctacttc cctctggcct aaggtagggg aggccttctc 3450
 agattgtggg gcacattgtg tagcctgact tctgctggag ctcccagtc 3500
 aggaggaaag agccaaggcc cacttttggg atcagggtgcc tgatcactgg 3550
 gccccctacc tcagcccccc tttccctgga gcacctgcc cacctgcccc 3600
 cagagaacac agtggctctc cctgtccggg ggcggctttt tcttctcttg 3650
 gagcgtccct gacggacaag tggaggcctc ttgctgcggc tgcaatggat 3700
 gcaaggggct gcagagccca ggtgcactgt gtgatgatgg gagggggctc 3750
 cgtcctgcag gctggagggt gcatccacac tggacagcag gaggggggga 3800
 gtgagggtaa catttccatt tcccttcatg ttttgtttct tacgttcttt 3850
 cagcatgctc cttaaaaccc cagaagcccc aatttcccca agccccattt 3900
 tttcttctct ttatctaata aactcaatat taag 3934

<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr

1

5

10

15

305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro Gly	
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro	
335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys Ala	
350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
365	370	

<210> 316
 <211> 4407
 <212> DNA
 <213> Homo sapiens

<400> 316
 cacagggaga cccacagaca catatgcacg agagagacag aggaggaaag 50
 agacagagac aaaggcacag cggaagaagg cagagacagg gcaggcacag 100
 aagcggccca gacagagtcc tacagaggga gaggccagag aagctgcaga 150
 agacacaggc agggagagac aaagatccag gaaaggaggg ctcaggagga 200
 gagtttgagg aagccagacc cctgggcacc tctcccaagc ccaaggacta 250
 agttttctcc atttccttta acggtcctca gcccttctga aaactttgcc 300
 tctgaccttg gcaggagtcc aagccccag gctacagaga ggagctttcc 350
 aaagctaggg tgtggaggac ttggtgccct agacggcctc agtccctccc 400
 agctgcagta ccagtgccat gtccagaca ggctcgcac cggggagggg 450
 cttggcaggg cgctggctgt ggggagccca accctgcctc ctgctcccca 500
 ttgtgccgct ctctggctg gtgtggctgc ttctgctact gctggcctct 550
 ctctgccct cagcccggct ggccagcccc ctccccggg aggaggagat 600
 cgtgtttcca gagaagctca acggcagcgt cctgcctggc tcgggogccc 650
 ctgccaggct gttgtgccgc ttgcaggcct ttggggagac gctgctacta 700
 gagctggagc aggactccgg tgtgcaggtc gaggggctga cagtgcagta 750
 cctgggccag gcgcctgagc tgctgggtgg agcagagcct ggcacctacc 800
 tgactggcac catcaatgga gatccggagt cgggtggcatc tctgcaactgg 850
 gatgggggag ccctgttagg cgtgttacaa tatcgggggg ctgaactcca 900
 cctccagccc ctggagggag gcaccctaa ctctgctggg ggacctgggg 950

ctcacatcct acgccggaag agtcctgcc a gcggtcaagg tcccatgtgc 1000
aacgtcaagg ctctctcttg aagccccagc cccagacccc gaagagccaa 1050
gcgctttgct tctactgagta gatttgtgga gacactgggtg gtggcagatg 1100
acaagatggc cgcattccac ggtgcggggc taaagcgcta cctgctaaca 1150
gtgatggcag cagcagccaa ggccttcaag cacccaagca tccgcaatcc 1200
tgtcagcttg gtggtgactc ggctagtgat cctgggggtca ggcgaggagg 1250
ggccccaagt ggggccaggt gctgccaga ccctgcgcag cttctgtgcc 1300
tggcagcggg gcctcaacac ccctgaggac tcgggccctg accactttga 1350
cacagccatt ctgtttaccc gtcaggacct gtgtggagtc tccacttgcg 1400
acacgctggg tatggctgat gtgggcaccg tctgtgaccc ggctcggagc 1450
tgtgccattg tggaggatga tgggctccag tcagccttca ctgctgctca 1500
tgaactgggt catgtcttca acatgtctca tgacaactcc aagccatgca 1550
tcagtttgaa tgggcctttg agcacctctc gccatgtcat ggccctgtg 1600
atggctcatg tggatcctga ggagccctgg tccccctgca gtgcccgtt 1650
catcactgac ttcttgaca atggctatgg gcactgtctc ttagacaaac 1700
cagaggctcc attgcatctg cctgtgactt tccctggcaa ggactatgat 1750
gctgaccgcc agtgccagct gaccttcggg cccgactcac gccattgtcc 1800
acagctgccg ccgccctgtg ctgccctctg gtgctctggc cacctcaatg 1850
gccatgccat gtgccagacc aaacactcgc cctgggccga tggcacaccc 1900
tgccggcccg cacaggcctg catgggtggg cgtgcctcc acatggacca 1950
gctccaggac ttcaatatc cacaggctgg tggctggggc ccttggggac 2000
catgggggtga ctgctctcg acctgtggg gtggtgtcca gttctctcc 2050
cgagactgca cgaggcctgt ccccggaat ggtggcaagt actgtgaggg 2100
ccgcgtacc cgcttcgct cctgcaacac tgaggactgc ccaactggct 2150
cagccctgac cttccgcgag gagcagtgtg ctgcctacaa ccaccgcacc 2200
gacctcttca agagcttccc agggcccatg gactgggttc ctgcctacac 2250
aggcgtggcc cccagagacc agtgcaaact cacctgccag gcccgggcac 2300
tgggctacta ctatgtgctg gagccacggg tggtagatgg gacccctgt 2350
tccccggaca gtcctcggg ctgtgtccag ggccgatgca tccatgctgg 2400

ctgtgatcgc atcattggct ccaagaagaa gtttgacaag tgcattggtgt 2450
gcgaggaggga cggttctggt tgcagcaagc agtcaggctc cttcaggaaa 2500
ttcagggtacg gatacaacaa tgtggtcact atccccgcgg gggccacca 2550
cattcttgtc cggcagcagg gaaaccctgg ccaccggagc atctacttgg 2600
ccctgaagct gccagatggc tcctatgccc tcaatggtga atacacgctg 2650
atgccctccc ccacagatgt ggtactgcct ggggcagtca gcttgcgcta 2700
cagcggggcc actgcagcct cagagacact gtcaggccat gggccactgg 2750
cccagccttt gacactgcaa gtccctagtgg ctggcaacct ccaggacaca 2800
cgcctccgat acagcttctt cgtgccccgg ccgacctt caacgccacg 2850
ccccactccc caggactggc tgcaccgaag agcacagatt ctggagatcc 2900
ttcggcggcg cccctgggcg ggcaggaaat aaacctacta tcccggctgc 2950
cctttctggg caccggggcc tcggacttag ctgggagaaa gagagagctt 3000
ctgttgctgc ctcatgctaa gactcagtgg ggaggggctg tgggcgtgag 3050
acctgcccct cctctctgcc ctaatgcgca ggttggccct gccctggttt 3100
cctgccctgg gaggcagtga tgggttagtg gatggaagg gctgacagac 3150
agccctccat ctaaactgcc ccctctgccc tgcgggtcac aggaggagg 3200
gggaaggcag ggagggcctg ggccccagtt gtatttattt agtatttatt 3250
cacttttatt tagcaccagg gaaggggaca aggactaggg tcctggggaa 3300
cctgaccctt gaccctcat agccctcacc ctggggctag gaaatccagg 3350
gtggtggtga taggtataag tggtgtgtgt atgctgtgtgt gtgtgtgtgt 3400
gaaaatgtgt gtgtgcttat gtatgaggta caacctgttc tgctttcctc 3450
ttcctgaatt ttattttttg ggaaaagaaa agtcaagggt aggggtgggc 3500
ttcagggagt gagggattat cttttttttt ttttctttct ttctttcttt 3550
tttttttttg agacagaatc tcgctctgtc gccaggctg gagtgaatg 3600
gcacaatctc ggctcactgc atcctccgcc tcccgggttc aagtgattct 3650
catgcctcag cctcctgagt agctgggatt acaggctcct gccaccacgc 3700
ccagctaatt tttgttttgt tttgtttgga gacagagtct cgctattgtc 3750
accagggctg gaatgatttc agctcactgc aaccttcgcc acctgggttc 3800
cagcaattct cctgcctcag cctcccaggt agctgagatt ataggcacct 3850

accaccacgc ccggctaatt tttgtatfff tagtagagac ggggtttcac 3900
catgtttggcc aggctggtct cgaactcctg accttaggtg atccactcgc 3950
cttcattctcc caaagtgctg ggattacagg cgtgagccac cgtgcctggc 4000
cacgccaac taatffffgt atffftagta gagacagggt ttcacatgt 4050
tggccaggct gctcttgaac tcctgacctc aggtaatoga cctgcctcgg 4100
cctcccaaag tgctgggatt acagggtgtga gccaccacgc ccggtacata 4150
ttttttaaat tgaattctac tatttatgtg atcctffttg agtcagacag 4200
atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250
ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300
aataaagaac tagcataaca ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400
aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg	1	5	10	15
Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro	20	25	30	
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	35	40	45		
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	50	55	60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	65	70	75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	80	85	90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	95	100	105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	110	115	120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	125	130	135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu				

Val	Thr	Phe	Pro	Gly 440	Lys	Asp	Tyr	Asp	Ala 445	Asp	Arg	Gln	Cys	Gln 450
Leu	Thr	Phe	Gly	Pro 455	Asp	Ser	Arg	His	Cys 460	Pro	Gln	Leu	Pro	Pro 465
Pro	Cys	Ala	Ala	Leu 470	Trp	Cys	Ser	Gly	His 475	Leu	Asn	Gly	His	Ala 480
Met	Cys	Gln	Thr	Lys 485	His	Ser	Pro	Trp	Ala 490	Asp	Gly	Thr	Pro	Cys 495
Gly	Pro	Ala	Gln	Ala 500	Cys	Met	Gly	Gly	Arg 505	Cys	Leu	His	Met	Asp 510
Gln	Leu	Gln	Asp	Phe 515	Asn	Ile	Pro	Gln	Ala 520	Gly	Gly	Trp	Gly	Pro 525
Trp	Gly	Pro	Trp	Gly 530	Asp	Cys	Ser	Arg	Thr 535	Cys	Gly	Gly	Gly	Val 540
Gln	Phe	Ser	Ser	Arg 545	Asp	Cys	Thr	Arg	Pro 550	Val	Pro	Arg	Asn	Gly 555
Gly	Lys	Tyr	Cys	Glu 560	Gly	Arg	Arg	Thr	Arg 565	Phe	Arg	Ser	Cys	Asn 570
Thr	Glu	Asp	Cys	Pro 575	Thr	Gly	Ser	Ala	Leu 580	Thr	Phe	Arg	Glu	Glu 585
Gln	Cys	Ala	Ala	Tyr 590	Asn	His	Arg	Thr	Asp 595	Leu	Phe	Lys	Ser	Phe 600
Pro	Gly	Pro	Met	Asp 605	Trp	Val	Pro	Arg	Tyr 610	Thr	Gly	Val	Ala	Pro 615
Gln	Asp	Gln	Cys	Lys 620	Leu	Thr	Cys	Gln	Ala 625	Arg	Ala	Leu	Gly	Tyr 630
Tyr	Tyr	Val	Leu	Glu 635	Pro	Arg	Val	Val	Asp 640	Gly	Thr	Pro	Cys	Ser 645
Pro	Asp	Ser	Ser	Ser 650	Val	Cys	Val	Gln	Gly 655	Arg	Cys	Ile	His	Ala 660
Gly	Cys	Asp	Arg	Ile 665	Ile	Gly	Ser	Lys	Lys 670	Lys	Phe	Asp	Lys	Cys 675
Met	Val	Cys	Gly	Gly 680	Asp	Gly	Ser	Gly	Cys 685	Ser	Lys	Gln	Ser	Gly 690
Ser	Phe	Arg	Lys	Phe 695	Arg	Tyr	Gly	Tyr	Asn 700	Asn	Val	Val	Thr	Ile 705
Pro	Ala	Gly	Ala	Thr 710	His	Ile	Leu	Val	Arg 715	Gln	Gln	Gly	Asn	Pro 720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

cagcagtggg ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtctgtttt 200
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc ccactctaatt atcagtttct gagttacaag 650
actttgagga ggaggagaa gatcttcact ttcttgcaa cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750
gaccgcgtac gccagacaag caagtgagga agaacttcca ataaatgact 800
atactgaaaa tggaaatagaa ttgatccca tgctggatga gagagggttat 850
tgttgatatt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcactctgtg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcattgtat tcaatgaatt tctgcctatg aggcatctgg 1100
cccttggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
1				5					10					15	
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50
cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100
ggcgtgacag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
tggcgctgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350
tgccctgctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
cacgcgctgc gccaaaggga caccgcgcaa gaccaccttt gccatccctg 450
gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550
cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
cgcccccttc gctcattggt ggcaccctgc tttgcctgtc ctgccaggac 650
gaggcaccct acaggcccta ccaggccccg cccaggggcca ccacgaccac 700
tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
gtccccggcg ggactgtcaa tggaggcagg ggttcagca caaagtttac 900
ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950
ctttagagca cagggaacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
 gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccgggt 150
 gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 200
 aaccccgctca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350
 gtcttgggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 500
 gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 gggggtgtga tgatgtgcat cgcttgcgg ggcttggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
 tccttccaag cagactatg tgtaatgctc taagacctct cagcacgggc 900
 ggaagaaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
 cccctcttc ctctagtca ataaacccat tgatgatcta tttccagot 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttotgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggtttttctt aactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaactt ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
 tcctctttct gtcgcggttc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggaggttg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1 5 10 15
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgttttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 tttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
 tcgccaatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50
 ctgggctggg tgaatggcct ggtctcctgt gccctgcca tgtggaaggt 100
 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
 gcctgtggat gtctgctgtg gtgcagagca ccggccagat gcagtgcagg 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgtctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgcctgggtgc tcacctctgg gattgtcttt gtcactctcag gggtcctgac 400
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg gggtgctgtg 550
 ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg gggtcgtacc 750
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgcca tcttagaagc cagtcaagct atggaactaa 950
 tgcggaggct gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
 agagtctctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gctgcccccc atctactca ggtctctgga gtcctctct tccccctgg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
 cagctatgta gacccccgc cccacctcca aactgcacc cttctgcct 1250

gccccctcg tctcaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
			20						25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
			35						40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
			50						55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
			65						70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
			80						85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
			95						100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
			110						115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
			125						130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
			140						145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
			155						160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
			170						175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
			185						190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
			200						205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
			215						220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtggg 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggctctcc cgcctgccct ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagaggg 450
ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
cacttttctt tggctgggca agcgtctgtg tcctcttcat tggagggggg 650
ctgctttgtg gattttgctg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaattgcct ccttttgggt 800
ccaagtatgg actatggtca atgttttita taaagtcctg ctagaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtttc aatttggttac tgggtgtagg aatgaaaatg acttacttgg 950
acattctgac ttcaggtgta ttaaattgat tgactattgt tggaccaat 1000
cgctgctcca attttcatat tctaaattca agtatacca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

ttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgcgcgca tggctgcctc cccgcgcgcg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaatth gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattgggc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggttttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct ttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
agccggggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gacccactgc ccagccgctc agggaccca acgcatccc agcccagcgc 250

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
50 55 60

Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
65 70 75

His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
80 85 90

Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
95 100 105

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
110 115 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
125 130 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
140 145 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
155 160 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
170 175 180

Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
185 190 195

Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
200 205 210

Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
215 220 225

Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
230 235 240

Phe Ala Met Tyr Arg Pro
245

<210> 339
<211> 849
<212> DNA
<213> Homo sapiens

<400> 339
gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50
tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
caagacccta agaaccatca gccctcagct gcacctctc ccctccaagg 150
atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcacccctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 345
 agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
 <211> 2575
 <212> DNA
 <213> Homo sapiens

<400> 346
 tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
 actgagaacc caccagctca tcccagacac ctcatagcaa cctattttata 100
 caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
 aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200
 gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
 ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
 ttgcacacgc tgttggtcaaa tgtcaggacc aggttaagtg actggcagaa 350
 aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
 gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttggcaa 450
 gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
 ctccagttcc tcctgctgct cctgatgctg ggatgcgtcc tgatgatggg 550
 ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
 aagccagcaa gcacagccct gaagccagggt accgcctgga ctttggggaa 650
 tcccaggatt gggacttgga agctgaggat gagggtgaag agtacagccc 700
 tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750
 tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800
 ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
 cccaaagagg gactgggggg ctgatgagga cggggagggt tctgaagaag 900
 aggagttgac cccgttcagc ctggaccac gtggcctcca ggaggcactc 950
 agtgcccgc tccccctcca gagggtctg cccgaggtgc ggcacccact 1000
 gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050
 tctgtttcca tgatgaggcc tgggtccact tcctgcggac tgtacacagc 1100

atcctcgaca cagtgccag gcccttcctg aaggagatca tctcgtgga 1150
cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200
ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250
atcagggccc ggatgctggg gccaccaga gccaccgggg atgtgctcgt 1300
cttcattgat gccactgcg agtgccaccc aggtgggtg gagccctcc 1350
tcagcagaat agctgggtgac aggagccgag tggatatctcc ggtgatagat 1400
gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450
tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500
atgtgaggaa ggccctccag tccccataa gcccacatcag gagccctgtg 1550
gtgcccggag aggtgggtggc catggacaga cattacttcc aaaacactgg 1600
agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctogaactgt 1650
ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tcctgctct 1700
cgggtaggac acatctacca aaatcaggat tccattccc ccctogacca 1750
ggaggccacc ctgaggaaca gggttcgcat tgctgagacc tggctggggt 1800
cattcaaaga aaccttctac aagcatagcc cagaggcctt ctcttgagc 1850
aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900
gggttgctcg acattccact ggtttctggc taatgtctac cctgagctgt 1950
acccatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000
cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050
catggtgttg gtccttgca gtgacagccg gcagcaacag tacctgcagc 2100
acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150
gctgtcaggc aggagcagg gattcttcag aactgcacgg aggaaggcct 2200
ggccatccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250
acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300
gatttgtagc tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350
tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400
aagagaattt tggccatcaa aatccagctc caagtgaacg taaagagctt 2450
atatatttca tgaagctgat ctttttgtgt gtgtgtcct tgtgttagga 2500
gagaaaaaag ctctatgaaa gaatatagga agtttctcct ttccacacct 2550

tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
1 5 10 15

Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly
260		265 270
Ala Thr Arg Ala Thr	Gly Asp Val Leu	Val Phe Met Asp Ala His
275		280 285
Cys Glu Cys His Pro	Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile
290		295 300
Ala Gly Asp Arg Ser	Arg Val Val Ser	Pro Val Ile Asp Val Ile
305		310 315
Asp Trp Lys Thr Phe	Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg
320		325 330
Gly Val Leu Asp Trp	Lys Leu Asp Phe	His Trp Glu Pro Leu Pro
335		340 345
Glu His Val Arg Lys	Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg
350		355 360
Ser Pro Val Val Pro	Gly Glu Val Val	Ala Met Asp Arg His Tyr
365		370 375
Phe Gln Asn Thr Gly	Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly
380		385 390
Gly Glu Asn Leu Glu	Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly
395		400 405
Ser Val Glu Ile Leu	Pro Cys Ser Arg	Val Gly His Ile Tyr Gln
410		415 420
Asn Gln Asp Ser His	Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg
425		430 435
Asn Arg Val Arg Ile	Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu
440		445 450
Thr Phe Tyr Lys His	Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala
455		460 465
Glu Lys Pro Asp Cys	Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu
470		475 480
Gly Cys Arg Thr Phe	His Trp Phe Leu	Ala Asn Val Tyr Pro Glu
485		490 495
Leu Tyr Pro Ser Glu	Pro Arg Pro Ser	Phe Ser Gly Lys Leu His
500		505 510
Asn Thr Gly Leu Gly	Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp
515		520 525
Ile Leu Gly Cys Pro	Met Val Leu Ala	Pro Cys Ser Asp Ser Arg
530		535 540
Gln Gln Gln Tyr Leu	Gln His Thr Ser	Arg Lys Glu Ile His Phe

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 350
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatacct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtgc 200
caggggaggg ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300
cctggcactg cacccccagc cccccatca ggctttgagg agggggccgcc 350
ctcatcccaa taccctgagg ctatcgtgtg ggggtccacc gtgtctcgag 400
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatggt 450
tttgagccc ctcatgggct cgcaaccca cccccaaact cagactccat 500
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600
gtcacaaatta ccatctccat catcattgtt ctctgtggca ctggcatcat 650
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
tccccggctg gagtactgt gctggggggc ttcggggact cacctacccc 800
caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850
acccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950
tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000
gcccctggcc ctcccaaggg ggctggacca gctcctctct gggaggcacc 1050
cttccttctc ccagtctctc aggatctgtg tcctattctc tgctgcccac 1100
aactccaact ctgccctctt tggttttttc tcatgccacc ttgtctaaga 1150
caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200
ttctattctg gcctacccct tggttcctga ctgtgccctt tccctcttcc 1250
tctcaggatt cccctggtga atctgtgatg cccccaatgt tgggggtgcag 1300

ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350
 ggcagctgtg gggagctggg gccacagggg ctcttggtc ctgccccttg 1400
 cacaccaccc ggaacactcc ccagcccac gggcaatcct atctgctcgc 1450
 cctcctgcag gtgggggcct cacatatctg tgacttcggg tccctgtccc 1500
 cacccttggt cactcacatg aaagccttgc aactcacct ccaccttcac 1550
 aggccatttg cacacgtcc tgcacctct ccccgccat accgctccgc 1600
 tcagctgact ctcatgttct ctctgtcac atttgcactc tctccttccc 1650
 acattctgtg ctgagctcac tcagtgggtca gcgtttcctg cacactttac 1700
 ctctcatgtg cgtttcccg gctgatgttg tgggtggtg cggcgtgctc 1750
 actctctccc tcatgaacac ccaccacct cgtttccgca gcccctgctg 1800
 gctgctccag aggtgggtgg gaggtgagct gggggctcct tgggccctca 1850
 tcgggtcatg tctcgtccca ttccacacca tttgtttctc tgtctcccca 1900
 tcctactcca aggatgccgg catcacctg agggctccc cttgggaatg 1950
 gggtagtgag gcccagact tcaccccag ccaactgcta aaatctgttt 2000
 tctgacagat gggttttggg gagtcgcctg ctgcactaca tgagaaagg 2050
 actcccatth gcccttccct ttctctaca gtcccttttg tcttgctgt 2100
 cctggctgtc tgtgtgtgtg ccattctctg gacttcagag cccctgagc 2150
 cagtcctccc ttcccagcct ccctttgggc ctccctaact ccacctaggc 2200
 tgccagggac cggagtcagc tggttcaagg ccatcgggag ctctgcctcc 2250
 aagtctaccc ttcccttccc ggaactccctc ctgtcccctc ctttccctcc 2300
 tccttccttc cactctcctt ccttttgctt ccctgccctt tccccctcct 2350
 caggttcttc cctccttctc actgggtttt ccaccttcct ccttcccttc 2400
 ttccctgggt cctagctgt gatatatatt tttgtattat ctctttcttc 2450
 ttcttggtgt gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500
 tcaaataaag cctttgcaag ataa 2524

<210> 352
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240
Leu Pro Lys																	

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcactcc 50

cggccaggat ggcacacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggccctcgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgcccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaagggggc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120
 Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
 ggccgttggt tgggtgcgcg ctgaagggtg tggcgcgagc agcgtcgttg 50
 gttggccggc ggcggggccg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactg cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcttgg 200
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400
catcttcgga gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550
agtagcccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tggcatcttc cagtacgaga ccattctctg caacaactgc acagactcgc 750
acgtcgcttg ctttggttat aactgcgagt agggctcagg catcacaccc 800
acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
gggctccccg ccttcacact ggctgtcatc gggtagggcg gggccgtggg 900
ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctggcgag 950
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100
ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150
gcggctgcag tccttttctc cctcaaaggc ctccgacct cagctggagg 1200
cgggcatctt tcctaaaggg tcccatagg gtctggttcc acccatccc 1250
aggtctgtgg tcagagcctg ggagggttcc ctacgatgg taggggtgcc 1300
ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350
tgaggttaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400
agaggagggg ggctagggg tcctctagat cagtgggggc actgcaggtg 1450
gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500
acccatgtgg tggtttcatg aacagaccac gtcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700
 cataggacca cacgtcccag ctgggaggag aggcctgggg cccccaggga 1750
 gggaggcagg ggggtggggga catggagagc tgaggcagcc tcgtctcccc 1800
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900
 gctgggcctg cccagggca acgtgggggc ggagactcag ctggacagcc 1950
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
1				5					10					15

His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
				20					25					30

Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
				35					40					45

Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
				50					55					60

Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
				65					70					75

Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
				80					85					90

Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
				95					100					105

Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
				110					115					120

Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln
				125					130					135

Leu	Ser	Arg	Glu	Gly	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Ser	Met	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatggt 50
cctcttattt ctcctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcagatggc cctgggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt ggggttattca acagcgtaat 500
tcagattcat ctcctcctga taatgaacaa ggcctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctcttttattc tgggtggacag tggtagaaa gaaaatggga aggtgatatc 650
atttttcaaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaato tcagagacac taaacaacag gatcactagg cctgccaaacc 950
acacacacac gcacgtgcac acacgcacgc acgctgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc totatgaaag agaggcattc 1200

ctagagaaag attgttccaa ttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tottttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser	
				200					205					210	
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr	
				215					220					225	
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val	
				230					235					240	
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly	
				245					250					255	
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys	
				260					265					270	

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagcaa 100
cctcagcggg gacccgggct cagggacgcg gcggcgggcg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactot 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtcct gtaaagagtc 850
tgcttcttgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200
atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400
tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattgg 1500
ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
<211> 269
<212> PRT
<213> Homo sapiens

<400> 364
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
20 25 30
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
35 40 45
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
50 55 60
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
65 70 75
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
80 85 90
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

```

gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctgggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgctc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggtctccgc 300
agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

```


Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			365	370	

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagagaa gtctgggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgacacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccgggcc gggactgggt cgcgaggggc 200
 tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
 tcaactgctc ggaaccagca ggatgggtacc ttgtccctgt cacagcggca 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctgggt gctatgtctc ctcccttgtc cctgcgtgct ccctgggtga 500
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtgggct gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
 agatggaaca ggcccagaag gccaagaacc ccaggagca gaagtccttc 750
 ttcgccaaat actggatgta catcattccc gtogtctgt tcctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttcagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgtcact tgatacgtta ttcagaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
 50 55 60
 Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
 65 70 75
 Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
 80 85 90
 Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
 95 100 105
 Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
 110 115 120
 Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
 125 130 135
 Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
 140 145 150
 Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
 155 160 165
 Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
 170 175 180
 Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
 185 190 195
 Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
 200 205 210
 Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
 215 220 225
 Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
 230 235 240
 Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
 245 250 255
 Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
 260 265

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgtgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttctc tcggtttcaa 250
ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctctttctc ctgacttact cactatgctg ctttaaccaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
ctgctcttct cagccttcga ggcttggtat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgccgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttctc ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cttttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgccctga gctgtaacct cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	
1				5					10					15	
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	
				20					25					30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	
				35					40					45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	
				50					55					60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	
				65					70					75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	
				80					85					90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	
				95					100					105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	
				110					115					120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	
				125					130					135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	
				140					145					150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	
				155					160					165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	
				170					175					180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	
				185					190					195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	
				200					205					210	
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tgggtcaagca agtgactggg aaaatgcccc toctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctgggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val	1	5	10	15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys	20	25	30	
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly	35	40	45	
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr	50	55	60	
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys	65	70	75	
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile	80	85	90	
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe	95	100	105	
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu	110	115						

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag ggggccagg agagtataaa 50

ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cagccttgcc 150

ctcctggggg gcccacctg ggccagggaag atgtatggc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagg gaaacttgga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450

tttggaagc ttgatggcca gatctcctct gcctaccca gccaaaggagg 500

gcagggtgtg gtgggcatct atggccagta tcaactcctt ggcatacaaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtgg 650

ggatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1					5				10				15	

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30

Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

atctcagaaa ttacaggaga taccctcaag tatactgtgt ggttgcttag 700
 gtttgtccct tcgtataaac agccttcaaa aacttaagta taatcaattt 750
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aaactggaac ttttgacact gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaaggtt ggtcagcctt 1200
 cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250
 gtccctggacc tggagctcct taaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggaccc agtggtttcc agtgtgtccc gaatctgcag 1350
 cgcccaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
 agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaaagta 1600
 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750
 totctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800
 ctgctcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900
 aaagacagtc cctaaagcaa atgactcca gcaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tcccccttccc 2150
 tctccctctc acttttggtgg caagatcctt ccttgtccgt tttagtgcac 2200
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
 1 5 10 15
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe
				215					220					225
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys
				230					235					240
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu
				245					250					255
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly
				260					265					270
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu
				275					280					285
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser
				290					295					300
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu
				305					310					315
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe
				320					325					330
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu
				335					340					345
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile
				350					355					360
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu
				365					370					375
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu
				380					385					390
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly
				395					400					405
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile
				410					415					420
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu
				425					430					435
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys
				440					445					450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys
				455					460					465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr
				470					475					480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu
				485					490					495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtcacctca 100
gcatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggacctt ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa	tggctggtat	atctggatcc	tcctgctgct	ggttttggtg	250
gcagctcttc	tctgtggagc	tgtggtcctc	tgcctccagt	gctggctgag	300
gagacccga	attgattctc	acaggcgcac	catggcagtt	tttgctgttg	350
gagacttgga	ctctatztat	gggacagaag	cagctgtgag	tccaactgtt	400
ggaattcacc	ttcaaactca	aacccctgac	ctatatcctg	ttcctgctcc	450
atgttttggc	cctttaggct	ccccacctcc	atatgaagaa	attgtaaaaa	500
caacctgatt	ttaggtgtgg	attatcaatt	taaagtatta	acgacatctg	550
taattccaaa	acatcaaatt	taggaatagt	tatttcagtt	gttggaatg	600
tccagagatc	tattcatata	gtctgaggaa	ggacaattcg	acaaaagaat	650
ggatgttgga	aaaaattttg	gtcatggaga	tgtttaaata	gtaaagtagc	700
aggcttttga	tgtgtcactg	ctgtatcata	cttttatgct	acacaaccaa	750
attaatgctt	ctccactagt	atccaaacag	gcaacaatta	ggtgctggaa	800
gtagtttcca	tcacatttag	gactccactg	cagtatacag	cacaccattt	850
tctgctttaa	actctttcct	agcatggggg	ccataaaaaat	tattataatt	900
taacaatagc	ccaagccgag	aatccaacat	gtccagaacc	agaaccagaa	950
agatagtatt	tgaatgaagg	tgaggggaga	gagtaggaaa	aagaaaagtt	1000
tggagttgaa	gggtaaagga	taaatgaaga	ggaaaaggaa	aagattacaa	1050
gtctcagcaa	aaacaagagg	ttttatgccc	caacctgaag	aggaagaaat	1100
tgtagataga	aggtgaagga	gattgctgaa	gatatagagc	acatataatg	1150
ccaacacggg	gagaaaagaa	aatttcccct	tttacagtaa	tgaatgtggc	1200
ctccatagtc	catagtgttt	ctctggagcc	tcagggcttg	gcattttattg	1250
cagcatcatg	ctaagaacct	tcggcatagg	tatctgttcc	catgaggact	1300
gcagaagtag	caatgagaca	tcttcaagtg	gcattttggc	agtggccatc	1350
agcaggggga	cagacaaaaa	catccatcac	agatgacata	tgatcttcag	1400
ctgacaaatt	tgttgaaaca	aacaataaac	atcaatagat	atctaaaaa	1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
1 5 10 15

5

10

15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

cttttcagtg tcacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacaccggc gtttctccag ctcgatctgg aggetgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttggt gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatgtggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtggg tgctcgagaac ggtgcttcta 650
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca cttgtgctg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950
aagctctaca catTTTcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aattttaaag ttatttggtt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 396

cgcgccggg cgcgggggt gagcgtgccg agggcggtgt ggcgaggct 50
 tccagcccc accatgccgt ggccctgct gctgctgctg gccgtgagt 100
 gggcccagac aaccggcca tgcttccccg ggtgccaatg cgagggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggttg attgtagcgg 200
 cctgggcccc cacatcatgc cgttgcccat ccctctggac acagccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc taccactg ccttctcccg ccttcgctac ctggagtcgc 400
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
 agctcaccct tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550
 acctctcca caacctcatt caccgcctcg tgccccaccc caccagggcc 600
 ggctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
atgggaaccc tctagctgtc attggtccgg gtgccttcgc ggggctggga 750
ggccttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800
gcccagtggc ttccgtgagc taccgggcct gcaggctcctg gacctgtcgg 850
gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggctgagc 900
tccctgcagg agctggacct ttcgggcacc aacctgggtgc ccctgcctga 950
ggcgctgtc ctccacctcc cggaactgca gagcgtcagc gtgggcccagg 1000
atgtgcggtg ccggcgccctg gtgcgggagg gcacctaccc ccggaggcct 1050
ggctccagcc ccaagggtgcc cctgcactgc gtagacaccc gggaatctgc 1100
tgccaggggc ccaccatct tgtgacaaat ggtgtggccc agggccacat 1150
aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200
tgtgccaaaca ccagtgggga gcccgcaggc ctatgtggca gcgtcaccac 1250
aggagttgtg ggcctaggag aggccttggga cctgggagcc acacctagga 1300
gcaaagtctc acccctttgt ctacgttgct tcccaaacc atgagcagag 1350
ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400
cttatccccc aagtgccttc cctcatgcct gggccggcct gaccgcgaat 1450
gggcagaggg tgggtgggac cccctgctgc agggcagagt tcaggtcac 1500
tgggctgagt gtccccttgg gcccatggcc cagtcaactca ggggcgagtt 1550
tcttttctaa catagccctt tctttgccat gaggccatga ggcccgttc 1600
atccttttct atttccctag aaccttaatg gtagaaggaa ttgcaaagaa 1650
tcaagtccac ccttctcatg tgacagatgg ggaaactgag gccttgagaa 1700
ggaaaaaggc taatctaagt tcctgcgggc agtggcatga ctggagcaca 1750
gcctcctgcc tcccagcccg gaccaatgc actttcttgt ctctctaat 1800
aagccccacc ctccccgcct gggctcccct tgctgccctt gcctgttccc 1850
cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900
gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgccc 1950
ttcggagcct ctggaagctt agggcacatt ggtccagcc tagccagttt 2000
ctcaccctgg gttgggggtcc ccagcatcc agactggaaa cctaccatt 2050
ttcccctgag catcctctag atgctgcccc aaggagttgc tgcagttctg 2100

gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150
ctggccctga gcacgacagc ctttcttacc ctcccaggaa tgccgtgaaa 2200
ggagacaagg tctgcccgcac ccatgtctat gctctacccc cagggcagca 2250
tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaag 2300
ttgttgccct tttaacggag tgtcactttc aaccggcctc ccctaccct 2350
gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaaggttgca 2400
tttgcttact tttgtaatat tgtcctgggc ctgtgttggg gtgttggggg 2450
aagctgggca tcagtggcca catgggcac aggggctggc cccacagaga 2500
ccccacaggg cagtgagctc tgtcttcccc cacctgccta gcccatcatc 2550
tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln	1	5	10	15
Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr	20	25	30	
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser	35	40	45	
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr	50	55	60	
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu	65	70	75	
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp	80	85	90	
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser	95	100	105	
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	110	115	120	
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp	125	130	135	
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala	140	145	150	

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttccoct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaaggg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttccoctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggtatTTaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggtcttc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gaggcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcacgac cccaaaccac catctcttta ctgtactagt 1000
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
 tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100
 atttttgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
 tttttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
 ctttaaaaaa attcacagat tatatttata acctgactag agcagggtgat 1250
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tttttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 402
 Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
 1 5 10 15
 Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
 20 25 30
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
 35 40 45
 Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
 50 55 60
 Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
 65 70 75
 Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
 80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgccat ttacagacac gtagtgattt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aaatcagtc ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgottgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgaccc cttggtcaat ggtgttctg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcggtgg cgtttgagga agctgggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

tgcacttata	tttttttagca	ctctgatcta	caaatttgga	agaaccgaag	600
agctatggac	ctgagatcac	ttcttaagtc	acatttttcct	tttgttatat	650
tctgtttgta	gatagggtttt	ttatctctca	gtacacattg	ccaaatggag	700
tagattgtac	attaaatggt	ttgtttcttt	acatttttat	gttctgagtt	750
ttgaaatagt	tttatgaaat	ttctttattt	ttcattgcat	agactgttaa	800
tatgtatata	atacaagact	atatgaattg	gataatgagt	atcagttttt	850
tattcctgag	atttagaact	tgatctactc	cctgagccag	ggttacatca	900
tcttgtcatt	ttagaagtaa	ccactcttgt	ctctctggct	gggcacggtg	950
gctcatgcct	gtaatcccag	cactttggga	ggccgaggcg	ggccgattgc	1000
ttgaggtcaa	gtgtttgaga	ccagcctggc	caacatggcg	aaaccccatc	1050
tactaaaaat	acaaaaatta	gccaggcatg	gtgggtgggtg	cctgtaatcc	1100
cagctacctg	ggaggctgag	gcaggagaat	cgcttgaacc	cggggggcag	1150
aggttgcagt	gagctgagtt	tgcgccactg	cactctagcc	tgggggagaa	1200
agtgaaactc	cctctcaaaa	aaaagaccac	tctcagtatc	tctgatttct	1250
gaagatgtac	aaaaaaatat	agcttcatat	atctggaatg	agcactgagc	1300
cataaaaggt	tttcagcaag	ttgtaaacta	ttttggccta	aaaatgaggt	1350
tttttttgta	aagaaaaaat	atttgttctt	atgtattgaa	gaagtgtact	1400
tttatataat	gatttttttaa	atgcccaaag	gactagtttg	aaagcttctt	1450
ttaaaaagaa	ttcctctaata	atgactttat	gtgagaa	1487	

<210> 410

<212> PRT

<213> Homo sapiens

<400> 410

Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1 5 10 15

Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
20 25 30

Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
35 40 45

Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60

Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtgggtggc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgtgggtt ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgttttaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctgggtg atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtg actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttaggggt gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaagggtgct 1100
gcaggctcct gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200
ctctctctct gctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggagggtg 300
atgttgatcc tggctgcaga tgggggtcaa cactggacgt atgaggggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactgggggc agaaaggatc ccaggggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc toacattgt acattatgac tctgattcct 700
atgacagctt gactgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgagggtgg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80					85					90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
 ggagagaggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
 cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcgggtctcct 100
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggtctccgc gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgct gagcgccctct gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttat tttt ggaccaagga agccctgaaa tgaattcaac 700
 aattaatatt catcgcactt cttctgtgga aggactttgt gaaggaattg 750
 gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
 ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
 tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
 ttattatgcc ttggaatggt tcaactaaat gacattttta ataagtttat 950
 gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt 1000
 tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
 aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
 acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
 aatttgtaaa tgtaagaat tttttttata tctgttaa at aaaaattatt 1250
 tccaaca 1257

<210> 431
 <211> 243
 <212> PRT
 <213> Homo Sapien

<400> 431
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
				230					235					240

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cccacctgta ccaccatgt 19

 <210> 436
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 actccaggca ccatctgttc tccc 24

 <210> 437
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 437
 aagggtggc attcaagtc 19

 <210> 438
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 438
 tgacctggca aaggaagaa 19

 <210> 439
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 439
 cagccaccct ccagtccaag g 21

 <210> 440
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 440
 gggtcgtggtt ttggagaga 19

 <210> 441
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 441
 ctggccctca gagcaccaat 20

 <210> 442
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 442
 tcctccatca cttcccctag ctcca 25

 <210> 443
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 443
 ctggcaggag ttaaagttcc aaga 24

 <210> 444
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 444
 aaaggacacc gggatgtg 18

 <210> 445
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 445
 agcgtacact ctctccaggc aaccag 26

 <210> 446
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 446
 caattctgga tgaggtggta ga 22

 <210> 447
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 447
 caggactgag cgcttggtta 20

 <210> 448
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 448
 caaagcgcca agtaccggac c 21

 <210> 449
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 449
 ccagacctca gccaggaa 18

 <210> 450
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 450
 ccctagctga ccccttca 18

<210> 451
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 451
 tctgacaagc agttttctga atc 23

 <210> 452
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 452
 ctctccccct cccttttctt ttgttt 26

 <210> 453
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 453
 ctctggtgcc cacagtga 18

 <210> 454
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 454
 ccatgcctgc tcagccaaga a 21

 <210> 455
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 455
 caggaaatct ggaaacctac agt 23

 <210> 456
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

ccttgaaaag gacccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457

atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458

tagcagctgc ccttggtta 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459

aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gcccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 472
tcagggtcta catcagcctc ctgc 24

<210> 473
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
aaggccaagg tgagtccat 19

<210> 474
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
cctactgagg agccctatgc 20

<210> 475
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
tccaggtgga cccacttca gg 22

<210> 476
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 476
gggaggctta taggccaat ctgg 24

<210> 477
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50